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<110> Ashkenazi, Avi J.
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Zhang, Zemin

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tggtaaaaat tgtaaaattaa aatgtcaac ttg 3033

<210> 6
<211> 251
<212> PRT
<213> Homo sapiens

<400> 6
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Arg Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly Lys
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Leu Gly Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala
35 40 45
Phe Leu Tyr Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe
50 55 60
Tyr Phe Pro Val Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn
65 70 75
Leu Tyr Phe Leu Tyr Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala
80 85 90
Phe Asp Gly Arg Pro Ala Asp Tyr Leu Phe Met Leu Leu Phe Asn
95 100 105

Trp Ile Cys Ile Val Ile Thr Gly Leu Ala Met Asp Met Gln Leu
110 115 120
Leu Met Ile Pro Leu Ile Met Ser Val Leu Tyr Val Trp Ala Gln
125 130 135
Leu Asn Arg Asp Met Ile Val Ser Phe Trp Phe Gly Thr Arg Phe
140 145 150
Lys Ala Cys Tyr Leu Pro Trp Val Ile Leu Gly Phe Asn Tyr Ile
155 160 165
Ile Gly Gly Ser Val Ile Asn Glu Leu Ile Gly Asn Leu Val Gly
170 175 180
His Leu Tyr Phe Phe Leu Met Phe Arg Tyr Pro Met Asp Leu Gly
185 190 195
Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe Leu Tyr Arg Trp Leu
200 205 210
Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly Val Pro Pro Ala
215 220 225
Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly Arg His
230 235 240
Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln
245 250

<210> 7
<211> 1373
<212> DNA
<213> Homo sapiens

<400> 7
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gtccggcggt ctggccctagg gatcttcccc ttggccctt tggggcgaaa 200
tggctgcggaa agaagaagac gaggtggagt gggtagtgga gagcatcgcg 250
gggttccctgc gaggcccaga ctggtccatc cccatcttg actttgtgga 300
acagaaaatg gaagtttaact gcaaaaggagg gcatgtgata actccaggaa 350
gcccgagacg ggtgatttt gtggccctgtt ttcccttgc ttttgtgtat 400
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aagatcaatt tcaagaagca tgcacttctc ctcttgcaaa gaccatcaca 550
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<210> 8
<211> 367
<212> PRT
<213> Homo sapiens

<400> 8
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Ile Ala Gly Phe Leu Arg Gly Pro Asp Trp Ser Ile Pro Ile Leu
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Asp Phe Val Glu Gln Lys Cys Glu Val Asn Cys Lys Gly Gly His
35 40 45
Val Ile Thr Pro Gly Ser Pro Glu Pro Val Ile Leu Val Ala Cys
50 55 60
Val Pro Leu Val Phe Asp Asp Glu Glu Ser Lys Leu Thr Tyr
65 70 75
Thr Glu Ile His Gln Glu Tyr Lys Glu Leu Val Glu Lys Leu Leu
80 85 90
Glu Gly Tyr Leu Lys Glu Ile Gly Ile Asn Glu Asp Gln Phe Gln
95 100 105
Glu Ala Cys Thr Ser Pro Leu Ala Lys Thr His Thr Ser Gln Ala
110 115 120
Ile Leu Gln Pro Val Leu Ala Ala Glu Asp Phe Thr Ile Phe Lys
125 130 135
Ala Met Met Val Gln Lys Asn Ile Glu Met Gln Leu Gln Ala Ile
140 145 150

Arg Ile Ile Gln Glu Arg Asn Gly Val Leu Pro Asp Cys Leu Thr
155 160 165
Asp Gly Ser Asp Val Val Ser Asp Leu Glu His Glu Glu Met Lys
170 175 180
Ile Leu Arg Glu Val Leu Arg Lys Ser Lys Glu Glu Tyr Asp Gln
185 190 195
Glu Glu Glu Arg Lys Arg Lys Lys Gln Leu Ser Glu Ala Lys Thr
200 205 210
Glu Glu Pro Thr Val His Ser Ser Glu Ala Ala Ile Met Asn Asn
215 220 225
Ser Gln Gly Asp Gly Glu His Phe Ala His Pro Pro Ser Glu Val
230 235 240
Lys Met His Phe Ala Asn Gln Ser Ile Glu Pro Leu Gly Arg Lys
245 250 255
Val Glu Arg Ser Glu Thr Ser Ser Leu Pro Gln Lys Gly Leu Lys
260 265 270
Ile Pro Gly Leu Glu His Ala Ser Ile Glu Gly Pro Ile Ala Asn
275 280 285
Leu Ser Val Leu Gly Thr Glu Glu Leu Arg Gln Arg Glu His Tyr
290 295 300
Leu Lys Gln Lys Arg Asp Lys Leu Met Ser Met Arg Lys Asp Met
305 310 315
Arg Thr Lys Gln Ile Gln Asn Met Glu Gln Lys Gly Lys Pro Thr
320 325 330
Gly Glu Val Glu Glu Met Thr Glu Lys Pro Glu Met Thr Ala Glu
335 340 345
Glu Lys Gln Thr Leu Leu Lys Arg Arg Leu Leu Ala Glu Lys Leu
350 355 360
Lys Glu Glu Val Ile Asn Lys
365

<210> 9
<211> 418
<212> DNA
<213> Homo sapiens

<400> 9
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aaggttacct caaagaaaatt ggaattaatg aagatcaatt tcaagaagca 150
tgcacttctc ctcttgcaaa gaccataaca tcacaggcca tttttgcaac 200
ctgtgttggc agcagaagat ttactatct ttaaagcaat gatggtccag 250
aaaaacattt aaatgcagct gcaagccatt cgaataattc aagagagaaa 300

tggtgttatta cctgactgct taaccgatgg ctctgatgtg gtcagtgacc 350
ttgaacacga agagataaa atcctgaggg aagttcttag aaaatcaaaa 400
gaggaatatg accaggaa 418

<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 10
ttgacctata cagagattca tc 22

<210> 11
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctaagaactt ccctcaggat ttt 23

<210> 12
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
atgaagatca atttcaagaa gcatgcactt ctccctttgc 40

<210> 13
<211> 2886
<212> DNA
<213> Homo sapiens

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caactagaac tcttctgagg gaggttaatta aaaaacagtg gaatggaaaa 200
acagtgcgtg agtcatcctg taatatgctc cttgtcaaca atgtatacat 250
tcctgtctgg tgccatattc attgtttaa gctcaagtgc catcttacta 300
gtgaagtatt ctgccaatga agaaaacaag tatgattatc ttccaactac 350
tgtaatgtg tgctcagaac tggtaagct agttttgtgt gtgttgtgt 400
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ttatccctcg gataacttga ttgtcttcta tgctctgtcc tatcttcaac 550
cagccatggc tggttatcttc tcaaattta gcattataac aacagcttt 600
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caatttgtaca gcaaaggaaat ggactttcc tgaagctaaa tggAACACCA 850
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ctttctaaa acgttgggtt aaggacctaa atacccggcc ataccataga 2000
tttggatgtc tgtagtctgt gctaaatatt ttgctgaaga agcagtttct 2050

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attttgtaa taatcttttgc atgttttaaa cattggttcc cttagtcacca 2150
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<210> 14
<211> 424
<212> PRT
<213> *Homo sapiens*

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<400> 14
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      1           5           10          15

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      20          25          30
      20          25          30

Ser Ser Arg Ile Leu Leu Val Lys Tyr Ser Ala Asn Glu Glu Asn
      35          40          45
      35          40          45

Lys Tyr Asp Tyr Leu Pro Thr Thr Val Asn Val Cys Ser Glu Leu
      50          55          60
      50          55          60

Val Lys Leu Val Phe Cys Val Leu Val Ser Phe Cys Val Ile Lys
      65          70          75
      65          70          75

Lys Asp His Gln Ser Arg Asn Leu Lys Tyr Ala Ser Trp Lys Glu
      80          85          90
      80          85          90

Phe Ser Asp Phe Met Lys Trp Ser Ile Pro Ala Phe Leu Tyr Phe
      95          100         105
      95          100         105

Leu Asp Asn Leu Ile Val Phe Tyr Val Leu Ser Tyr Leu Gln Pro
      110          115         120
      110          115         120

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CDS

Ala Met Ala Val Ile Phe Ser Asn Phe Ser Ile Ile Thr Thr Ala
 125 130 135
 Leu Leu Phe Arg Ile Val Leu Lys Arg Arg Leu Asn Trp Ile Gln
 140 145 150
 Trp Ala Ser Leu Leu Thr Leu Phe Leu Ser Ile Val Ala Leu Thr
 155 160 165
 Ala Gly Thr Lys Thr Leu Gln His Asn Leu Ala Gly Arg Gly Phe
 170 175 180
 His His Asp Ala Phe Phe Ser Pro Ser Asn Ser Cys Leu Leu Phe
 185 190 195
 Arg Ser Glu Cys Pro Arg Lys Asp Asn Cys Thr Ala Lys Glu Trp
 200 205 210
 Thr Phe Pro Glu Ala Lys Trp Asn Thr Thr Ala Arg Val Phe Ser
 215 220 225
 His Ile Arg Leu Gly Met Gly His Val Leu Ile Ile Val Gln Cys
 230 235 240
 Phe Ile Ser Ser Met Ala Asn Ile Tyr Asn Glu Lys Ile Leu Lys
 245 250 255
 Glu Gly Asn Gln Leu Thr Glu Ser Ile Phe Ile Gln Asn Ser Lys
 260 265 270
 Leu Tyr Phe Phe Gly Ile Leu Phe Asn Gly Leu Thr Leu Gly Leu
 275 280 285
 Gln Arg Ser Asn Arg Asp Gln Ile Lys Asn Cys Gly Phe Phe Tyr
 290 295 300
 Gly His Ser Ala Phe Ser Val Ala Leu Ile Phe Val Thr Ala Phe
 305 310 315
 Gln Gly Leu Ser Val Ala Phe Ile Leu Lys Phe Leu Asp Asn Met
 320 325 330
 Phe His Val Leu Met Ala Gln Val Thr Thr Val Ile Ile Thr Thr
 335 340 345
 Val Ser Val Leu Val Phe Asp Phe Arg Pro Ser Leu Glu Phe Phe
 350 355 360
 Leu Glu Ala Pro Ser Val Leu Leu Ser Ile Phe Ile Tyr Asn Ala
 365 370 375
 Ser Lys Pro Gln Val Pro Glu Tyr Ala Pro Arg Gln Glu Arg Ile
 380 385 390
 Arg Asp Leu Ser Gly Asn Leu Trp Glu Arg Ser Ser Gly Asp Gly
 395 400 405
 Glu Glu Leu Glu Arg Leu Thr Lys Pro Lys Ser Asp Glu Ser Asp
 410 415 420
 Glu Asp Thr Phe

<210> 15
<211> 755
<212> DNA
<213> Homo sapiens

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tactacgggg ctagacagtt actgtcttagt ctcttagatg tgcgttcttc 200
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ctttta 755

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
ctatacctac ttagtcttcc 20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcagagaatt cttccagga 20

<210> 18
<211> 40
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 18

acagtgcgtg agtcatcctg taatatgctc cttgtcaaca 40

<210> 19

<211> 2142

<212> DNA

<213> Homo sapiens

<400> 19

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ggccgcgtgc gggcagagga gcatcccgtc taccagggtcc caagcggcgt 150

ggccgcgggg tcatggccaa aggagaaggc gccgagagcg gctccgcgc 200

ggggctgcta cccaccagca tcctccaaag cactgaacgc cggcccccagg 250

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ggaactttgtt ctgttttgc acctacacct tgggcttccg caatgaattc 1150

cagaatctac tcctggccat catgtctcg gccactttaa ccattcccat 1200

ctggcagtgg ttcttgaccc ggtttggcaa gaagacagct gtatatgtt 1250

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<210> 20
<211> 458
<212> PRT
<213> *Homo sapiens*

Glu Arg Asp Ser Ala Thr Ala Tyr Arg Met Thr Val Glu Val Leu
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 Gly Thr Val Leu Gly Thr Ala Ile Gln Gly Gln Ile Val Gly Gln
 125 130 135
 Ala Asp Thr Pro Cys Phe Gln Asp Phe Asn Ser Ser Thr Val Ala
 140 145 150
 Ser Gln Ser Ala Asn His Thr His Gly Thr Thr Ser His Arg Glu
 155 160 165
 Thr Gln Lys Ala Tyr Leu Leu Ala Ala Gly Val Ile Val Cys Ile
 170 175 180
 Tyr Ile Ile Cys Ala Val Ile Leu Ile Leu Gly Val Arg Glu Gln
 185 190 195
 Arg Glu Pro Tyr Glu Ala Gln Gln Ser Glu Pro Ile Ala Tyr Phe
 200 205 210
 Arg Gly Leu Arg Leu Val Met Ser His Gly Pro Tyr Ile Lys Leu
 215 220 225
 Ile Thr Gly Phe Leu Phe Thr Ser Leu Ala Phe Met Leu Val Glu
 230 235 240
 Gly Asn Phe Val Leu Phe Cys Thr Tyr Thr Leu Gly Phe Arg Asn
 245 250 255
 Glu Phe Gln Asn Leu Leu Leu Ala Ile Met Leu Ser Ala Thr Leu
 260 265 270
 Thr Ile Pro Ile Trp Gln Trp Phe Leu Thr Arg Phe Gly Lys Lys
 275 280 285
 Thr Ala Val Tyr Val Gly Ile Ser Ser Ala Val Pro Phe Leu Ile
 290 295 300
 Leu Val Ala Leu Met Glu Ser Asn Leu Ile Ile Thr Tyr Ala Val
 305 310 315
 Ala Val Ala Ala Gly Ile Ser Val Ala Ala Ala Phe Leu Leu Pro
 320 325 330
 Trp Ser Met Leu Pro Asp Val Ile Asp Asp Phe His Leu Lys Gln
 335 340 345
 Pro His Phe His Gly Thr Glu Pro Ile Phe Phe Ser Phe Tyr Val
 350 355 360
 Phe Phe Thr Lys Phe Ala Ser Gly Val Ser Leu Gly Ile Ser Thr
 365 370 375
 Leu Ser Leu Asp Phe Ala Gly Tyr Gln Thr Arg Gly Cys Ser Gln
 380 385 390
 Pro Glu Arg Val Lys Phe Thr Leu Asn Met Leu Val Thr Met Ala
 395 400 405
 Pro Ile Val Leu Ile Leu Leu Gly Leu Leu Phe Lys Met Tyr
 410 415 420

Pro Ile Asp Glu Glu Arg Arg Arg Gln Asn Lys Lys Ala Leu Gln
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Ala Leu Arg Asp Glu Ala Ser Ser Ser Gly Cys Ser Glu Thr Asp
440 445 450
Ser Thr Glu Leu Ala Ser Ile Leu
455

<210> 21
<211> 571
<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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cttccttcag cccttgcataat ttggacatctt gctgtttca tattttcata 200
cattactgcata gtaacactcc accatataga cccggcttta ccttataatca 250
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ctggcccttgc ttttggataat ctgagttgtt taggactttc tattttggca 450

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gataatcagg aaacatgaaa gaagccattt gatagattat tctaaaggat 1100
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gaaaataaaag tcaaaagact atg 1173

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<211> 266
<212> PRT
<213> Homo sapiens

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Val Thr Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp
35 40 45
Thr Gly Thr Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu
50 55 60
Asn Ile Ala Ala Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr
65 70 75
Lys Gln Val His Ala Leu Ser Pro Glu Glu Asn Val Ile Ile Lys
80 85 90
Leu Asn Lys Ala Gly Leu Val Leu Gly Ile Leu Ser Cys Leu Gly
95 100 105
Leu Ser Ile Val Ala Asn Phe Gln Lys Thr Thr Leu Phe Ala Ala
110 115 120
His Val Ser Gly Ala Val Leu Thr Phe Gly Met Gly Ser Leu Tyr
125 130 135

Met Phe Val Gln Thr Ile Leu Ser Tyr Gln Met Gln Pro Lys Ile
140 145 150

His Gly Lys Gln Val Phe Trp Ile Arg Leu Leu Leu Val Ile Trp
155 160 165

Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys Ser Ser Val Leu
170 175 180

His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys Leu His Trp
185 190 195

Asn Pro Glu Asp Lys Gly Tyr Val Leu His Met Ile Thr Thr Ala
200 205 210

Ala Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu Thr
215 220 225

Tyr Ile Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn
230 235 240

Leu His Gly Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn
245 250 255

Asn Glu Arg Thr Arg Leu Leu Ser Arg Asp Ile
260 265

<210> 24
<211> 485
<212> DNA
<213> Homo sapiens

<220>
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<222> 14, 484
<223> unknown base

<400> 24
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gagcggagat cctcaaaccg cctagtgttc cgegcttccg gagaaaatca 150
gcggctaat taattccctt ggtttgttga agcagttacc aagaatcttc 200
aaccctttcc cacaaaagct aattgagttac acgttccctgt tgtagtacacg 250
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gcaaggccctt agttcccttc cttcagccctt tgtaatttgg acatctgtctg 400
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gctttacatt atatcagtgttga cactggtaca gtanc 485

<210> 25
<211> 40
<212> DNA
<213> Artificial Sequence

Ergonomics

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cacttggga ggccgaggcc ggtgattcac aaggtcagga gttcaagacc 1200
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<210> 28
<211> 264
<212> PRT
<213> Homo sapiens

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Phe Ala Leu Tyr Leu Leu Ser Thr Arg Leu Pro Arg Gly Arg Arg
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35 40 45
Ser Asp Leu Ala Glu Leu Arg Glu Leu Ser Glu Val Leu Arg Glu
50 55 60
Tyr Arg Lys Glu His Gln Ala Tyr Val Phe Leu Leu Phe Cys Gly
65 70 75
Ala Tyr Leu Tyr Lys Gln Gly Phe Ala Ile Pro Gly Ser Ser Phe
80 85 90
Leu Asn Val Leu Ala Gly Ala Leu Phe Gly Pro Trp Leu Gly Leu
95 100 105
Leu Leu Cys Cys Val Leu Thr Ser Val Gly Ala Thr Cys Cys Tyr
110 115 120
Leu Leu Ser Ser Ile Phe Gly Lys Gln Leu Val Val Ser Tyr Phe
125 130 135
Pro Asp Lys Val Ala Leu Leu Gln Arg Lys Val Glu Glu Asn Arg
140 145 150
Asn Ser Leu Phe Phe Leu Leu Phe Leu Arg Leu Phe Pro Met
155 160 165
Thr Pro Asn Trp Phe Leu Asn Leu Ser Ala Pro Ile Leu Asn Ile
170 175 180
Pro Ile Val Gln Phe Phe Ser Val Leu Ile Gly Leu Ile Pro
185 190 195
Tyr Asn Phe Ile Cys Val Gln Thr Gly Ser Ile Leu Ser Thr Leu
200 205 210

Thr Ser Leu Asp Ala Leu Phe Ser Trp Asp Thr Val Phe Lys Leu
215 220 225
Leu Ala Ile Ala Met Val Ala Leu Ile Pro Gly Thr Leu Ile Lys
230 235 240
Lys Phe Ser Gln Lys His Leu Gln Leu Asn Glu Thr Ser Thr Ala
245 250 255
Asn His Ile His Ser Arg Lys Asp Thr
260

<210> 29
<211> 1292
<212> DNA
<213> Homo sapiens

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tggaaagacat ggatcttgct gccaacgaga tcagcattta tgacaaactt 200
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tttcagccca ttagcacctg agccagtctt ttctggagct cacacctggc 450
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 gaaagggaa aaataaaaac aaaaacgatg aaactgcaa aa 1292

 <210> 30
 <211> 347
 <212> PRT
 <213> Homo sapiens

 <400> 30
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 Ser Glu Lys Ala Ile Glu Lys Phe Ile Arg Gln Leu Leu Glu Lys
 35 40 45
 Asn Glu Pro Gln Arg Pro Pro Pro Gln Tyr Pro Leu Leu Ile Val
 50 55 60
 Val Tyr Lys Val Leu Ala Thr Leu Gly Leu Ile Leu Leu Thr Ala
 65 70 75
 Tyr Phe Val Ile Gln Pro Phe Ser Pro Leu Ala Pro Glu Pro Val
 80 85 90
 Leu Ser Gly Ala His Thr Trp Arg Ser Leu Ile His His Ile Arg
 95 100 105
 Leu Met Ser Leu Pro Ile Ala Lys Lys Tyr Met Ser Glu Asn Lys
 110 115 120
 Gly Val Pro Leu His Gly Gly Asp Glu Asp Arg Pro Phe Pro Asp
 125 130 135
 Phe Asp Pro Trp Trp Thr Asn Asp Cys Glu Gln Asn Glu Ser Glu
 140 145 150
 Pro Ile Pro Ala Asn Cys Thr Gly Cys Ala Gln Lys His Leu Lys
 155 160 165
 Val Met Leu Leu Glu Asp Ala Pro Arg Lys Phe Glu Arg Leu His
 170 175 180
 Pro Leu Val Ile Lys Thr Gly Lys Pro Leu Leu Glu Glu Glu Ile
 185 190 195
 Gln His Phe Leu Cys Gln Tyr Pro Glu Ala Thr Glu Gly Phe Ser
 200 205 210
 Glu Gly Phe Phe Ala Lys Trp Trp Arg Cys Phe Pro Glu Arg Trp
 215 220 225
 Phe Pro Phe Pro Tyr Pro Trp Arg Arg Pro Leu Asn Arg Ser Gln
 230 235 240
 Met Leu Arg Glu Leu Phe Pro Val Phe Thr His Leu Pro Phe Pro
 245 250 255

Homo sapiens

Lys Asp Ala Ser Leu Asn Lys Cys Ser Phe Leu His Pro Glu Pro
260 265 270
Val Val Gly Ser Lys Met His Lys Met Pro Asp Leu Phe Ile Ile
275 280 285
Gly Ser Gly Glu Ala Met Leu Gln Leu Ile Pro Pro Phe Gln Cys
290 295 300
Arg Arg His Cys Gln Ser Val Ala Met Pro Ile Glu Pro Gly Asp
305 310 315
Ile Gly Tyr Val Asp Thr Thr His Trp Lys Val Tyr Val Ile Ala
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Arg Gly Val Gln Pro Leu Val Ile Cys Asp Gly Thr Ala Phe Ser
335 340 345

Glu Leu

<210> 31
<211> 478
<212> DNA
<213> Homo sapiens

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<211> 3531
<212> DNA
<213> Homo sapiens

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gcagagcgct gctcctggct ggtgccactg gtgcgcacgc tgctagaccc 150
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ggggccgccc tgagggccag cactggcgtc t 3531

<210> 33
<211> 1003
<212> PRT
<213> Homo sapiens

<400> 33
Met Ser Gln Phe Glu Met Asp Thr Tyr Ala Lys Ser His Asp Leu
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Met Ser Gly Phe Trp Asn Ala Cys Tyr Asp Met Leu Met Ser Ser
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Gly Gln Arg Arg Gln Trp Glu Arg Ala Gln Ser Arg Arg Ala Phe
35 40 45

Gln Glu Leu Val Leu Glu Pro Ala Gln Arg Arg Ala Arg Leu Glu
50 55 60

Gly Leu Arg Tyr Thr Ala Val Leu Lys Gln Gln Ala Thr Gln His
65 70 75

Ser Met Ala Leu Leu His Trp Gly Ala Leu Trp Arg Gln Leu Ala
80 85 90

Ser Pro Cys Gly Ala Trp Ala Leu Arg Asp Thr Pro Ile Pro Arg
95 100

Trp Lys Leu Ser Ser Ala Glu Thr Tyr Ser Arg Met Arg Leu Lys
110 115 120

Leu Val Pro Asn His His Phe Asp Pro His Leu Glu Ala Ser Ala
125 130 135

Leu Arg Asp Asn Leu Gly Glu Val Pro Leu Thr Pro Thr Glu Glu
140 145 150

Ala Ser Leu Pro Leu Ala Val Thr Lys Glu Ala Lys Val Ser Thr
155 160 165

Pro Pro Glu Leu Leu Gln Glu Asp Gln Leu Gly Glu Asp Glu Leu
170 175 180

Ala Glu Leu Glu Thr Pro Met Glu Ala Ala Glu Leu Asp Glu Gln
185 190 195

Arg Glu Lys Leu Val Leu Ser Ala Glu Cys Gln Leu Val Thr Val
200 205 210

Val Ala Val Val Pro Gly Leu Leu Glu Val Thr Thr Gln Asn Val
215 220 225

Tyr Phe Tyr Asp Gly Ser Thr Glu Arg Val Glu Thr Glu Glu Gly
230 235 240

Ile Gly Tyr Asp Phe Arg Arg Pro Leu Ala Gln Leu Arg Glu Val
245 250 255

His Leu Arg Arg Phe Asn Leu Arg Arg Ser Ala Leu Glu Leu Phe
260 265 270

Phe	Ile	Asp	Gln	Ala	Asn	Tyr	Phe	Leu	Asn	Phe	Pro	Cys	Lys	Val
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Gly	Thr	Thr	Pro	Val	Ser	Ser	Pro	Ser	Gln	Thr	Pro	Arg	Pro	Gln
				290					295					300
Pro	Gly	Pro	Ile	Pro	Pro	His	Thr	Gln	Val	Arg	Asn	Gln	Val	Tyr
				305					310					315
Ser	Trp	Leu	Leu	Arg	Leu	Arg	Pro	Pro	Ser	Gln	Gly	Tyr	Leu	Ser
				320					325					330
Ser	Arg	Ser	Pro	Gln	Glu	Met	Leu	Arg	Ala	Ser	Gly	Leu	Thr	Gln
				335					340					345
Lys	Trp	Val	Gln	Arg	Glu	Ile	Ser	Asn	Phe	Glu	Tyr	Leu	Met	Gln
				350					355					360
Leu	Asn	Thr	Ile	Ala	Gly	Arg	Thr	Tyr	Asn	Asp	Leu	Ser	Gln	Tyr
				365					370					375
Pro	Val	Phe	Pro	Trp	Val	Leu	Gln	Asp	Tyr	Val	Ser	Pro	Thr	Leu
				380					385					390
Asp	Leu	Ser	Asn	Pro	Ala	Val	Phe	Arg	Asp	Leu	Ser	Lys	Pro	Ile
				395					400					405
Gly	Val	Val	Asn	Pro	Lys	His	Ala	Gln	Leu	Val	Arg	Glu	Lys	Tyr
				410					415					420
Glu	Ser	Phe	Glu	Asp	Pro	Ala	Gly	Thr	Ile	Asp	Lys	Phe	His	Tyr
				425					430					435
Gly	Thr	His	Tyr	Ser	Asn	Ala	Ala	Gly	Val	Met	His	Tyr	Leu	Ile
				440					445					450
Arg	Val	Glu	Pro	Phe	Thr	Ser	Leu	His	Val	Gln	Leu	Gln	Ser	Gly
				455					460					465
Arg	Phe	Asp	Cys	Ser	Asp	Arg	Gln	Phe	His	Ser	Val	Ala	Ala	Ala
				470					475					480
Trp	Gln	Ala	Arg	Leu	Glu	Ser	Pro	Ala	Asp	Val	Lys	Glu	Leu	Ile
				485					490					495
Pro	Glu	Phe	Phe	Tyr	Phe	Pro	Asp	Phe	Leu	Glu	Asn	Gln	Asn	Gly
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Phe	Asp	Leu	Gly	Cys	Leu	Gln	Leu	Thr	Asn	Glu	Lys	Val	Gly	Asp
				515					520					525
Val	Val	Leu	Pro	Pro	Trp	Ala	Ser	Ser	Pro	Glu	Asp	Phe	Ile	Gln
				530					535					540
Gln	His	Arg	Gln	Ala	Leu	Glu	Ser	Glu	Tyr	Val	Ser	Ala	His	Leu
				545					550					555
His	Glu	Trp	Ile	Asp	Leu	Ile	Phe	Gly	Tyr	Lys	Gln	Arg	Gly	Pro
				560					565					570
Ala	Ala	Glu	Glu	Ala	Leu	Asn	Val	Phe	Tyr	Tyr	Cys	Thr	Tyr	Glu
				575					580					585

TOP + SBTG69

Gly	Ala	Val	Asp	Leu	Asp	His	Val	Thr	Asp	Glu	Arg	Glu	Arg	Lys
				590					595					600
Ala	Leu	Glu	Gly	Ile	Ile	Ser	Asn	Phe	Gly	Gln	Thr	Pro	Cys	Gln
				605					610					615
Leu	Leu	Lys	Glu	Pro	His	Pro	Thr	Arg	Leu	Ser	Ala	Glu	Glu	Ala
				620					625					630
Ala	His	Arg	Leu	Ala	Arg	Leu	Asp	Thr	Asn	Ser	Pro	Ser	Ile	Phe
				635					640					645
Gln	His	Leu	Asp	Glu	Leu	Lys	Ala	Phe	Phe	Ala	Glu	Val	Thr	Val
				650					655					660
Ser	Ala	Ser	Gly	Leu	Leu	Gly	Thr	His	Ser	Trp	Leu	Pro	Tyr	Asp
				665					670					675
Arg	Asn	Ile	Ser	Asn	Tyr	Phe	Ser	Phe	Ser	Lys	Asp	Pro	Thr	Met
				680					685					690
Gly	Ser	His	Lys	Thr	Gln	Arg	Leu	Leu	Ser	Gly	Pro	Trp	Val	Pro
				695					700					705
Gly	Ser	Gly	Val	Ser	Gly	Gln	Ala	Leu	Ala	Val	Ala	Pro	Asp	Gly
				710					715					720
Lys	Leu	Leu	Phe	Ser	Gly	Gly	His	Trp	Asp	Gly	Ser	Leu	Arg	Val
				725					730					735
Thr	Ala	Leu	Pro	Arg	Gly	Lys	Leu	Leu	Ser	Gln	Leu	Ser	Cys	His
				740					745					750
Leu	Asp	Val	Val	Thr	Cys	Leu	Ala	Leu	Asp	Thr	Cys	Gly	Ile	Tyr
				755					760					765
Leu	Ile	Ser	Gly	Ser	Arg	Asp	Thr	Thr	Cys	Met	Val	Trp	Arg	Leu
				770					775					780
Leu	His	Gln	Gly	Gly	Leu	Ser	Val	Gly	Leu	Ala	Pro	Lys	Pro	Val
				785					790					795
Gln	Val	Leu	Tyr	Gly	His	Gly	Ala	Ala	Val	Ser	Cys	Val	Ala	Ile
				800					805					810
Ser	Thr	Glu	Leu	Asp	Met	Ala	Val	Ser	Gly	Ser	Glu	Asp	Gly	Thr
				815					820					825
Val	Ile	Ile	His	Thr	Val	Arg	Arg	Gly	Gln	Phe	Val	Ala	Ala	Leu
				830					835					840
Arg	Pro	Leu	Gly	Ala	Thr	Phe	Pro	Gly	Pro	Ile	Phe	His	Leu	Ala
				845					850					855
Leu	Gly	Ser	Glu	Gly	Gln	Ile	Val	Val	Gln	Ser	Ser	Ala	Trp	Glu
				860					865					870
Arg	Pro	Gly	Ala	Gln	Val	Thr	Tyr	Ser	Leu	His	Leu	Tyr	Ser	Val
				875					880					885
Asn	Gly	Lys	Leu	Arg	Ala	Ser	Leu	Pro	Leu	Ala	Glu	Gln	Pro	Thr
				890					895					900

Ala Leu Thr Val Thr Glu Asp Phe Val Leu Leu Gly Thr Ala Gln
905 910 915
Cys Ala Leu His Ile Leu Gln Leu Asn Thr Leu Leu Pro Ala Ala
920 925 930
Pro Pro Leu Pro Met Lys Val Ala Ile Arg Ser Val Ala Val Thr
935 940 945
Lys Glu Arg Ser His Val Leu Val Gly Leu Glu Asp Gly Lys Leu
950 955 960
Ile Val Val Val Ala Gly Gln Pro Ser Glu Val Arg Ser Ser Gln
965 970 975
Phe Ala Arg Lys Leu Trp Arg Ser Ser Arg Arg Ile Ser Gln Val
980 985 990
Ser Ser Gly Glu Thr Glu Tyr Asn Pro Thr Glu Ala Arg
995 1000

<210> 34

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

tgactgcact accccgtggc aagctgtta gccagtcgtc ctg 43

<210> 35

<211> 1395

<212> DNA

<213> Homo sapiens

<400> 35

cggacgcgtg ggccggacgcg tgggggtgtt gaaaaatgc caataataac 50

atcatgcac cccacggccc accttgtaa ctcctcgat ccaggcgtt 100

tgtgcgtttt ccagggttac tcatccaaat gcctaattca acgttctgtc 150

ttcaatctgc aaatctatgg ggtcctgggg ctcttcttgc cccttaactg 200

ggtaactggcc ctgggccaat ggttcctcgat tggagccttt gcttccttct 250

actgggcctt ccacaagcccc caggacatcc ctacccccc cttaatctct 300

gccttcattcc gcacactcc ttaccacact ggttcattgg cattttggac 350

ccttcattcc acccttgtgc agatagcccg ggttcatttg gatgtatgg 400

accacaagct cagaggatgc cagaaccctg tagcccgctg catcatgtgc 450

tgtttcaagt gctgcctctg gtgtctggaa aaattttatca agttcctaaa 500

ccgcaatgcata catatcatga tgcgcattctt cggaaagaat ttctgtgtct 550

cagccaaaaa tgcggttcatgc ctactcatgc gaaacattgt cagggtggtc 600

gtccctggaca aagtccacaga cctgtctgtc ttctttggaa agctgtgtgt 650

ggtcggaggc gtgggggtcc tgtccttott tttttctcc ggtcgcattcc 700
cggggctggg taaagacttt aagagcccc acctcaacta ttactggctg 750
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cagcgtttc gcatgtgtg tggacacgtt cttectctgc ttcccttgaag 850
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ccagccgtgc caacatggtg aaacctccgt ctctattaaa aatacaaaaa 1200
ttagccgaga gtgggtggcat gcacctgtca tcccagctac tcgggaggct 1250
gaggcaggag aatcgcttga acccgggagg cagaggttc agtgagccg 1300
gatcgcgcaca ctgcactcca acctgggtga cagactctgt ctccaaaaca 1350
aaacaaacaa acaaaaagat ttatattaaag atatttgtt aactc 1395

<210> 36
<211> 321
<212> PRT
<213> Homo sapiens

<400> 36
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Pro Gly Leu Met Cys Val Phe Gln Gly Tyr Ser Ser Lys Gly Leu
35 40 45
Ile Gln Arg Ser Val Phe Asn Leu Gln Ile Tyr Gly Val Leu Gly
50 55 60
Leu Phe Trp Thr Leu Asn Trp Val Leu Ala Leu Gly Gln Cys Val
65 70 75
Leu Ala Gly Ala Phe Ala Ser Phe Tyr Trp Ala Phe His Lys Pro
80 85 90
Gln Asp Ile Pro Thr Phe Pro Leu Ile Ser Ala Phe Ile Arg Thr
95 100 105
Leu Arg Tyr His Thr Gly Ser Leu Ala Phe Gly Ala Leu Ile Leu
110 115 120
Thr Leu Val Gln Ile Ala Arg Val Ile Leu Glu Tyr Ile Asp His
125 130 135

Lys Leu Arg Gly Val Gln Asn Pro Val Ala Arg Cys Ile Met Cys
140 145 150

Cys Phe Lys Cys Cys Leu Trp Cys Leu Glu Lys Phe Ile Lys Phe
155 160 165

Leu Asn Arg Asn Ala Tyr Ile Met Ile Ala Ile Tyr Gly Lys Asn
170 175 180

Phe Cys Val Ser Ala Lys Asn Ala Phe Met Leu Leu Met Arg Asn
185 190 195

Ile Val Arg Val Val Val Leu Asp Lys Val Thr Asp Leu Leu Leu
200 205 210

Phe Phe Gly Lys Leu Leu Val Val Gly Gly Val Gly Val Leu Ser
215 220 225

Phe Phe Phe Ser Gly Arg Ile Pro Gly Leu Gly Lys Asp Phe
230 235 240

Lys Ser Pro His Leu Asn Tyr Tyr Trp Leu Pro Ile Met Thr Ser
245 250 255

Ile Leu Gly Ala Tyr Val Ile Ala Ser Gly Phe Phe Ser Val Phe
260 265 270

Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe Leu Glu Asp Leu
275 280 285

Glu Arg Asn Asn Gly Ser Leu Asp Arg Pro Tyr Tyr Met Ser Lys
290 295 300

Ser Leu Leu Lys Ile Leu Gly Lys Lys Asn Glu Ala Pro Pro Asp
305 310 315

Asn Lys Lys Arg Lys Lys
320

<210> 37

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 37

tcgtgccccag gggctgtatgt gc 22

<210> 38

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 38

gtctttaccc agccccggga tgcg 24

<210> 39

<211> 50

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 39
ggccataatcc aacgttctgt cttaaatctg caaatctatg gggtcctggg 50

<210> 40
<211> 1365
<212> DNA
<213> Homo sapiens

<400> 40
gagtcttgac cgccgcggg ctcttggtag ctcagcgaga ggcgcaggcg 50
tcggccgcg gttggatgtatgt tcgtgtccaa ttccgcggaa gagttctacg 100
agggtgtccaa gagcccgagg gtccttcgt tcgtggcctc ggacgtggat 150
gctctgtgtc cgtgcaagat ctttcaggcc ttgttccagt gtgaccacgt 200
gcaataatacg ctgggtcccg tttctgggtg gcaagaactt gaaactgtcat 250
ttcttgagca taaaagaacag tttcattatt ttattctcat aaactgtgga 300
gctaataatgtt acctattggaa tattcttcaa cctgtatggaa acactatatt 350
ctttgtgtc gactcccata ggcagtcgtt cttgtcaat gtataacaacg 400
atacccgat caaattactt attaaacaag atgatgaccc tgaagttccc 450
gccttatggaa acatcttcag ggatggaaag gaggatggaa agcattcagg 500
aaatgacagt gatgggttcg agccttcgtaa gaagcgccaca cggttagaaag 550
aggagatagt ggagcaaacccatgcggagga ggcagcgccg agagttggag 600
gccccggagaa gagacatccctt ctttgactac gagcgtatg aatatcatgg 650
gacatcgta gccatggta tgtttggact ggcttggatg ctgtccaagg 700
acctgtatgtt catgtgtgg tggccatcg ttggactaaac agaccagtgg 750
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cactctccgtt ggactgcaca cggatctcc tttagtatgtt cttccgcctg 900
gtgtcttacc agcaactggc cttccatgc acgctgtca acaccagcta 950
tacccgagcc aggttcaage tttgtgtctgtt gcatggacag aacgcggctcc 1000
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agatgttgc aataaaatggt ggatggaggat catgcgcgtg cagactttca 1150
gcatttattttt tgggttcaag cacaaggtttcc tggccagcgaa cgtggcttt 1200
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gccaccatgt ctttgatgga gagcccgag aaggatggct cagggacaga 1250
tcaccttcac caggctctgg acagcctctc caggagtaac ctggacaagc 1300
tgttacatgg ccttggaaactc gccaagaagc agctgcgagc cacccagcag 1350
accatttgcac gctgc 1365

<210> 41
<211> 566
<212> PRT
<213> Homo sapiens

<400> 41
Met Phe Val Ser Asp Phe Arg Lys Glu Phe Tyr Glu Val Val Gln
1 5 10 15
Ser Gln Arg Val Leu Leu Phe Val Ala Ser Asp Val Asp Ala Leu
20 25 30
Cys Ala Cys Lys Ile Leu Gln Ala Leu Phe Gln Cys Asp His Val
35 40 45
Gln Tyr Thr Leu Val Pro Val Ser Gly Trp Gln Glu Leu Glu Thr
50 55 60
Ala Phe Leu Glu His Lys Glu Gln Phe His Tyr Phe Ile Leu Ile
65 70 75
Asn Cys Gly Ala Asn Val Asp Leu Leu Asp Ile Leu Gln Pro Asp
80 85 90
Glu Asp Thr Ile Phe Phe Val Cys Asp Ser His Arg Pro Val Asn
95 100 105
Val Val Asn Val Tyr Asn Asp Thr Gln Ile Lys Leu Leu Ile Lys
110 115 120
Gln Asp Asp Asp Leu Glu Val Pro Ala Tyr Glu Asp Ile Phe Arg
125 130 135
Asp Glu Glu Glu Asp Glu Glu His Ser Gly Asn Asp Ser Asp Gly
140 145 150
Ser Glu Pro Ser Glu Lys Arg Thr Arg Leu Glu Glu Glu Ile Val
155 160 165
Glu Gln Thr Met Arg Arg Arg Gln Arg Arg Glu Trp Glu Ala Arg
170 175 180
Arg Arg Asp Ile Leu Phe Asp Tyr Glu Gln Tyr Glu Tyr His Gly
185 190 195
Thr Ser Ser Ala Met Val Met Phe Glu Leu Ala Trp Met Leu Ser
200 205 210
Lys Asp Leu Asn Asp Met Leu Trp Trp Ala Ile Val Gly Leu Thr
215 220 225
Asp Gln Trp Val Gln Asp Lys Ile Thr Gln Met Lys Tyr Val Thr
230 235 240
Asp Val Gly Val Leu Gln Arg His Val Ser Arg His Asn His Arg

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	245	250	255
Asn Glu Asp Glu Glu Asn Thr Leu Ser Val Asp Cys Thr Arg Ile	260	265	270
Ser Phe Glu Tyr Asp Leu Arg Leu Val Leu Tyr Gln His Trp Ser	275	280	285
Leu His Asp Ser Leu Cys Asn Thr Ser Tyr Thr Ala Ala Arg Phe	290	295	300
Lys Leu Trp Ser Val His Gly Gln Lys Arg Leu Gln Glu Phe Leu	305	310	315
Ala Asp Met Gly Leu Pro Leu Lys Gln Val Lys Gln Lys Phe Gln	320	325	330
Ala Met Asp Ile Ser Leu Lys Glu Asn Leu Arg Glu Met Ile Glu	335	340	345
Glu Ser Ala Asn Lys Phe Gly Met Lys Asp Met Arg Val Gln Thr	350	355	360
Phe Ser Ile His Phe Gly Phe Lys His Lys Phe Leu Ala Ser Asp	365	370	375
Val Val Phe Ala Thr Met Ser Leu Met Glu Ser Pro Glu Lys Asp	380	385	390
Gly Ser Gly Thr Asp His Phe Ile Gln Ala Leu Asp Ser Leu Ser	395	400	405
Arg Ser Asn Leu Asp Lys Leu Tyr His Gly Leu Glu Leu Ala Lys	410	415	420
Lys Gln Leu Arg Ala Thr Gln Gln Thr Ile Ala Ser Cys Leu Cys	425	430	435
Thr Asn Leu Val Ile Ser Gln Gly Pro Phe Leu Tyr Cys Ser Leu	440	445	450
Met Glu Gly Thr Pro Asp Val Met Leu Phe Ser Arg Pro Ala Ser	455	460	465
Leu Ser Leu Leu Ser Lys His Leu Leu Lys Ser Phe Val Cys Ser	470	475	480
Thr Lys Asn Arg Arg Cys Lys Leu Leu Pro Leu Val Met Ala Ala	485	490	495
Pro Leu Ser Met Glu His Gly Thr Val Thr Val Val Gly Ile Pro	500	505	510
Pro Glu Thr Asp Ser Ser Asp Arg Lys Asn Phe Phe Gly Arg Leu	515	520	525
Phe Glu Lys Ala Ala Glu Ser Thr Ser Ser Arg Met Leu His Asn	530	535	540
His Phe Asp Leu Ser Val Ile Glu Leu Lys Ala Glu Asp Arg Ser	545	550	555
Lys Phe Leu Asp Ala Leu Ile Ser Leu Leu Ser			

<210> 42
<211> 380
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 44, 118, 172, 183
<223> unknown base

<400> 42
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ctcttcgtgg cctcggangt ggatgcctgt tgtgcgtca agatccttca 150
ggccttggttc cagtgtgacc angtgaata tangctggtt ccagttctg 200
ggtgtgcaaga acttggaaact gcatttcttg agcataaaga acagtttcat 250
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tcaacacctgtat gaagacacta tattttttgt gtgtgacacc cataggccag 350
tcaatgttgtt caatgtatac aacgataccc 380

<210> 43
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
ttccgcaaaag agttctacga ggtgg 25

<210> 44
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 44
attgacaaca ttgactggcc tatggg 26

<210> 45
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 45
gtggatgctc tgtgtgcgtg caagatcctt caggccttgc tccagtgta 50

<210> 46

<211> 3089
<212> DNA
<213> Homo sapiens

<400> 46
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tttctagtga accacgaagg gacgatacca gaaaacaccc tcaacccaaa 100
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gagtcaagaa accccccctt cttgagctat ttacagcttt taacaattga 250
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taaagaatgc tgtctccctc tggaaaaaaaaaaaaaaaaaa 3089

<210> 47
<211> 259
<212> PRT
<213> Homo sapiens

<220>
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<222> 1-20
<223> Signal Peptide

<220>
<221> N-glycosylation Site
<222> 72-75
<223> N-glycosylation Site

<220>
<221> C1q Domain Proteins
<222> 144-178, 78-111, 84-117
<223> C1q Domain Proteins

<400> 47
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20 25 30 35
Arg Ala Val Ala Ser Gly Cys Gln Arg Cys Cys Asp Ser Glu Asp
35 40 45
Pro Leu Asp Pro Ala His Val Ser Ser Ala Ser Ser Ser Gly Arg
50 55 60
Pro His Ala Leu Pro Glu Ile Arg Pro Tyr Ile Asn Ile Thr Ile
65 70 75
Leu Lys Gly Asp Lys Gly Asp Pro Gly Pro Met Gly Leu Pro Gly
80 85 90
Tyr Met Gly Arg Glu Gly Pro Gln Gly Glu Pro Gly Pro Gln Gly
95 100 105
Ser Lys Gly Asp Lys Gly Glu Met Gly Ser Pro Gly Ala Pro Cys
110 115 120
Gln Lys Arg Phe Phe Ala Phe Ser Val Gly Arg Lys Thr Ala Leu
125 130 135
His Ser Gly Glu Asp Phe Gln Thr Leu Leu Phe Glu Arg Val Phe
140 145 150
Val Asn Leu Asp Gly Cys Phe Asp Met Ala Thr Gly Gln Phe Ala
155 160 165
Ala Pro Leu Arg Gly Ile Tyr Phe Phe Ser Leu Asn Val His Ser
170 175 180
Trp Asn Tyr Lys Glu Thr Tyr Val His Ile Met His Asn Gln Lys
185 190 195
Glu Ala Val Ile Leu Tyr Ala Gln Pro Ser Glu Arg Ser Ile Met

200 205 210
Gln Ser Gln Ser Val Met Leu Asp Leu Ala Tyr Gly Asp Arg Val
215 220 225
Trp Val Arg Leu Phe Lys Arg Gln Arg Glu Asn Ala Ile Tyr Ser
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Ala Glu Asp Asp

<210> 48

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48

ccagacgctg ctttcgaaa gggtc 25

<210> 49

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 49

ggtccccgtt ggccagggtc agc 23

<210> 50

<211> 50

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 50

ctacttcttc agcctcaatg tgcacagctg gaattacaag gagacgtacg 50

<210> 51

<211> 2768

<212> DNA

<213> Homo sapiens

<400> 51

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tgctcctgt actggccctg gggctgggg tgcaaggctg cccatccggc 200

tgccagtgca gcaaggccaca gagacttcc tgactgccc gccaggggac 250

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<210> 52

<211> 673

<212> PRT

<213> Homo sapiens

<400> 52
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Ser Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr
35 40 45
Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe
50 55 60
Glu Asn Gly Ile Thr Met Leu Asp Ala Gly Ser Phe Ala Gly Leu
65 70 75
Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser
80 85 90
Leu Pro Ser Gly Val Phe Gln Pro Leu Ala Asn Leu Ser Asn Leu

95	100	105
Asp Leu Thr Ala Asn Arg Leu His Glu Ile Thr Asn Glu Thr Phe		
110	115	120
Arg Gly Leu Arg Arg Leu Glu Arg Leu Tyr Leu Gly Lys Asn Arg		
125	130	135
Ile Arg His Ile Gln Pro Gly Ala Phe Asp Thr Leu Asp Arg Leu		
140	145	150
Leu Glu Leu Lys Leu Gln Asn Glu Leu Arg Ala Leu Pro Pro		
155	160	165
Leu Arg Leu Pro Arg Leu Leu Leu Asp Leu Ser His Asn Ser		
170	175	180
Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu		
185	190	195
Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp Glu Gly		
200	205	210
Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser Asp		
215	220	225
Asn Gln Leu Glu Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly		
230	235	240
Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu		
245	250	255
Arg Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp		
260	265	270
Val Ser Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly		
275	280	285
Leu Phe Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe		
290	295	300
Asn Cys Val Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu		
305	310	315
Ser His Val Thr Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe		
320	325	330
Pro Pro Lys Asn Ala Gly Arg Leu Leu Leu Glu Leu Asp Tyr Ala		
335	340	345
Asp Phe Gly Cys Pro Ala Thr Thr Thr Ala Thr Val Pro Thr		
350	355	360
Thr Arg Pro Val Val Arg Glu Pro Thr Ala Leu Ser Ser Ser Leu		
365	370	375
Ala Pro Thr Trp Leu Ser Pro Thr Ala Pro Ala Thr Glu Ala Pro		
380	385	390
Ser Pro Pro Ser Thr Ala Pro Pro Thr Val Gly Pro Val Pro Gln		
395	400	405
Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn Gly Gly Thr Cys		

410	415	420
His Leu Gly Thr Arg His His Leu Ala Cys	Leu Cys Pro Glu	Gly
425	430	435
Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met	Gly Gln Gly Thr Arg	
440	445	450
Pro Ser Pro Thr Pro Val Thr Pro Arg Pro	Pro Arg Ser Leu Thr	
455	460	465
Leu Gly Ile Glu Pro Val Ser Pro Thr Ser	Leu Arg Val Gly	Leu
470	475	480
Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln	Leu Arg Ser Leu Arg	
485	490	495
Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp	Lys Arg Leu Val Thr	
500	505	510
Leu Arg Leu Pro Ala Ser Leu Ala Glu Tyr	Thr Val Thr Gln Leu	
515	520	525
Arg Pro Asn Ala Thr Tyr Ser Val Cys Val	Met Pro Leu Gly Pro	
530	535	540
Gly Arg Val Pro Glu Gly Glu Ala Cys	Gly Glu Ala His Thr	
545	550	555
Pro Pro Ala Val His Ser Asn His Ala Pro	Val Thr Gln Ala Arg	
560	565	570
Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro	Ala Leu Ala Ala Val	
575	580	585
Leu Leu Ala Ala Leu Ala Ala Val Gly	Ala Ala Tyr Cys Val Arg	
590	595	600
Arg Gly Arg Ala Met Ala Ala Ala Gln Asp	Lys Gly Gln Val	
605	610	615
Gly Pro Gly Ala Gly Pro Leu Glu Leu Glu	Gly Val Lys Val Pro	
620	625	630
Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly	Gly Glu Ala Leu	
635	640	645
Pro Ser Gly Ser Glu Cys Glu Val Pro Leu	Met Gly Phe Pro Gly	
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Pro Gly Leu Gln Ser Pro Leu His Ala Lys	Pro Tyr Ile	
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<210> 53

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 53

tcttcagccg cttgcgcAAC ctc 23

<210> 54
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 54
ttgctcacat ccagctcctg cagg 24

<210> 55
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 55
tggatgttgt ccagacaacc agctggagct gtatccgagg c 41

<210> 56
<211> 3462
<212> DNA
<213> Homo sapiens

<400> 56
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tggaaataca atgagactca tcagaaacat ttacatattt tgtagtattt 150
ttatgacago agagggtgat gctccagagc tgccagaaga aaggaaactg 200
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agagttcaga ttttatttcgt ctccaaac tgagatttt gattctatgc 350
cataacagaa ttcaacagct ggatctcaa accttgaat tcaacaaggaa 400
gttaagatattt ttagattttt ctaataacag actgaagagt gtaacttgg 450
atttactggc aggtctcagg tatttagatc ttcttttaa tgactttgac 500
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tttgggtgta aggTTtatCT tgaccacaAT tcatttgact actcaaaTAC 1000
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ctgacaatAT caaatGCACA aatGCCACAC atgcTTTCC cgaATTATCC 1150
tagaaATTc caatTTTAa atTTTGCAA taatATCTTA acagACGAGT 1200
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gaACCCATTc CATTCTATTG CATTCCCACc AGGTATCATA aACTGAAAGC 2350
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gccaccAGAG aATGTATGA ACTGCAcAGAcA tTCACAGAGT tAAATGAAGA 2500

TOP SECRET

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<210> 57

<211> 811

<212> PRT

<213> Homo sapiens

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					20				25				30	
Met	Thr	Asn	Cys	Ser	Asn	Met	Ser	Leu	Arg	Lys	Val	Pro	Ala	Asp
						35			40				45	
Leu	Thr	Pro	Ala	Thr	Thr	Leu	Asp	Leu	Ser	Tyr	Asn	Leu	Leu	
						50			55				60	
Phe	Gln	Leu	Gln	Ser	Ser	Asp	Phe	His	Ser	Val	Ser	Lys	Leu	Arg
						65			70				75	
Val	Leu	Ile	Leu	Cys	His	Asn	Arg	Ile	Gln	Gln	Leu	Asp	Leu	Lys
						80			85				90	

Thr	Phe	Glu	Phe	Asn	Lys	Glu	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	Asn
					95					100				105
Asn	Arg	Leu	Lys	Ser	Val	Thr	Trp	Tyr	Leu	Leu	Ala	Gly	Leu	Arg
					110					115				120
Tyr	Leu	Asp	Leu	Ser	Phe	Asn	Asp	Phe	Asp	Thr	Met	Pro	Ile	Cys
					125					130				135
Glu	Glu	Ala	Gly	Asn	Met	Ser	His	Leu	Glu	Ile	Leu	Gly	Leu	Ser
					140					145				150
Gly	Ala	Lys	Ile	Gln	Lys	Ser	Asp	Phe	Gln	Lys	Ile	Ala	His	Leu
					155					160				165
His	Leu	Asn	Thr	Val	Phe	Leu	Gly	Phe	Arg	Thr	Leu	Pro	His	Tyr
					170					175				180
Glu	Glu	Gly	Ser	Leu	Pro	Ile	Leu	Asn	Thr	Thr	Lys	Leu	His	Ile
					185					190				195
Val	Leu	Pro	Met	Asp	Thr	Asn	Phe	Trp	Val	Leu	Leu	Arg	Asp	Val
					200					205				210
Ile	Lys	Thr	Ser	Lys	Ile	Leu	Glu	Met	Thr	Asn	Ile	Asp	Gly	Lys
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Ser	Gln	Phe	Val	Ser	Tyr	Glu	Met	Gln	Arg	Asn	Leu	Ser	Leu	Glu
					230					235				240
Asn	Ala	Lys	Thr	Ser	Val	Leu	Leu	Leu	Asn	Lys	Val	Asp	Leu	Leu
					245					250				255
Trp	Asp	Asp	Leu	Phe	Leu	Ile	Leu	Gln	Phe	Val	Trp	His	Thr	Ser
					260					265				270
Val	Glu	His	Phe	Gln	Ile	Arg	Asn	Val	Thr	Phe	Gly	Gly	Lys	Ala
					275					280				285
Tyr	Leu	Asp	His	Asn	Ser	Phe	Asp	Tyr	Ser	Asn	Thr	Val	Met	Arg
					290					295				300
Thr	Ile	Lys	Leu	Glu	His	Val	His	Phe	Arg	Val	Phe	Tyr	Ile	Gln
					305					310				315
Gln	Asp	Lys	Ile	Tyr	Leu	Leu	Leu	Thr	Lys	Met	Asp	Ile	Glu	Asn
					320					325				330
Leu	Thr	Ile	Ser	Asn	Ala	Gln	Met	Pro	His	Met	Leu	Phe	Pro	Asn
					335					340				345
Tyr	Pro	Thr	Lys	Phe	Gln	Tyr	Leu	Asn	Phe	Ala	Asn	Ile	Leu	
					350					355				360
Thr	Asp	Glu	Leu	Phe	Lys	Arg	Thr	Ile	Gln	Leu	Pro	His	Leu	Lys
					365					370				375
Thr	Leu	Ile	Leu	Asn	Gly	Asn	Lys	Leu	Glu	Thr	Leu	Ser	Leu	Val
					380					385				390
Ser	Cys	Phe	Ala	Asn	Asn	Thr	Pro	Leu	Glu	His	Leu	Asp	Leu	Se
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Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn Cys Ser Trp Pro
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 Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu Asp Leu
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 Asn Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His Leu
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 470 475 480
 Leu Pro Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile
 485 490 495
 Glu Met Asn Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser
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 515 520 525
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 530 535 540
 Glu Val Met Met Val Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr
 545 550 555
 Pro Leu Asn Leu Arg Gly Thr Arg Leu Lys Asp Val His Leu His
 560 565 570
 Glu Leu Ser Cys Asn Thr Ala Leu Leu Ile Val Thr Ile Val Val
 575 580 585
 Ile Met Leu Val Leu Gly Leu Ala Val Ala Phe Cys Cys Leu His
 590 595 600
 Phe Asp Leu Pro Trp Tyr Leu Arg Met Leu Gly Gln Cys Thr Gln
 605 610 615
 Thr Trp His Arg Val Arg Lys Thr Thr Gln Glu Gln Leu Lys Arg
 620 625 630
 Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser Glu His Asp Ser
 635 640 645
 Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp
 650 655 660
 Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly
 665 670 675
 Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser Tyr
 680 685 690
 Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp
 695 700 705
 Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu
 710 715 720

Asn Ser Asp His Ile Ile Leu Leu Leu Glu Pro Ile Pro Phe
725 730 735

Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu Lys Ala Leu Leu Glu
740 745 750

Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly
755 760 765

Leu Phe Trp Ala Asn Leu Arg Ala Ala Ile Asn Val Asn Val Leu
770 775 780

Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn
785 790 795

Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp Cys
800 805 810

Leu

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 59
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 59
ttatagacaa tctgttctca tcagaga 27

<210> 60
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 60
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<210> 61
<211> 3772
<212> DNA
<213> Homo sapiens

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THE TURKISH

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<211> 756
<212> PRT
<213> Homo sapiens

<400> 62
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Glu Asp Pro Asp Tyr Tyr Gly Gln Glu Ile Trp Ser Arg Glu Pro
35 40 45
Tyr Tyr Ala Arg Pro Glu Pro Glu Leu Glu Thr Phe Ser Pro Pro
50 55 60
Leu Pro Ala Gly Pro Gly Glu Glu Trp Glu Arg Arg Pro Gln Glu
65 70 75
Pro Arg Pro Pro Lys Arg Ala Thr Lys Pro Lys Lys Ala Pro Lys
80 85 90
Arg Glu Lys Ser Ala Pro Glu Pro Pro Pro Gly Lys His Ser
95 100 105
Asn Lys Lys Val Met Arg Thr Lys Ser Ser Glu Lys Ala Ala Asn
110 115 120
Asp Asp His Ser Val Arg Val Ala Arg Glu Asp Val Arg Glu Ser
125 130 135
Cys Pro Pro Leu Gly Leu Glu Thr Leu Lys Ile Thr Asp Phe Gln
140 145 150
Leu His Ala Ser Thr Val Lys Arg Tyr Gly Leu Gly Ala His Arg
155 160 165
Gly Arg Leu Asn Ile Gln Ala Gly Ile Asn Glu Asn Asp Phe Tyr
170 175 180
Asp Gly Ala Trp Cys Ala Gly Arg Asn Asp Leu Gln Gln Trp Ile

185 190 195

Glu	Val	Asp	Ala	Arg	Arg	Leu	Thr	Arg	Phe	Thr	Gly	Val	Ile	Thr
200									205					210
Gln	Gly	Arg	Asn	Ser	Leu	Trp	Leu	Ser	Asp	Trp	Val	Thr	Ser	Tyr
215									220					225
Lys	Val	Met	Val	Ser	Asn	Asp	Ser	His	Thr	Trp	Val	Thr	Val	Lys
230									235					240
Asn	Gly	Ser	Gly	Asp	Met	Ile	Phe	Glu	Gly	Asn	Ser	Glu	Lys	Glu
245									250					255
Ile	Pro	Val	Leu	Asn	Glu	Leu	Pro	Val	Pro	Met	Val	Ala	Arg	Tyr
260									265					270
Ile	Arg	Ile	Asn	Pro	Gln	Ser	Trp	Phe	Asp	Asn	Gly	Ser	Ile	Cys
275									280					285
Met	Arg	Met	Glu	Ile	Leu	Gly	Cys	Pro	Leu	Pro	Asp	Pro	Asn	Asn
290									295					300
Tyr	Tyr	His	Arg	Arg	Asn	Glu	Met	Thr	Thr	Thr	Asp	Asp	Leu	Asp
305									310					315
Phe	Lys	His	His	Asn	Tyr	Lys	Glu	Met	Arg	Gln	Leu	Met	Lys	Val
320									325					330
Val	Asn	Glu	Met	Cys	Pro	Asn	Ile	Thr	Arg	Ile	Tyr	Asn	Ile	Gly
335									340					345
Lys	Ser	His	Gln	Gly	Leu	Lys	Leu	Tyr	Ala	Val	Glu	Ile	Ser	Asp
350									355					360
His	Pro	Gly	Glu	His	Glu	Val	Gly	Glu	Pro	Glu	Phe	His	Tyr	Ile
365									370					375
Ala	Gly	Ala	His	Gly	Asn	Glu	Val	Leu	Gly	Arg	Glu	Leu	Leu	Leu
380									385					390
Leu	Leu	Val	Gln	Phe	Val	Cys	Gln	Glu	Tyr	Leu	Ala	Arg	Asn	Ala
395									400					405
Arg	Ile	Val	His	Leu	Val	Glu	Glu	Thr	Arg	Ile	His	Val	Leu	Pro
410									415					420
Ser	Leu	Asn	Pro	Asp	Gly	Tyr	Glu	Lys	Ala	Tyr	Glu	Gly	Ser	
425										430				435
Glu	Leu	Gly	Gly	Trp	Ser	Leu	Gly	Arg	Trp	Thr	His	Asp	Gly	Ile
440									445					450
Asp	Ile	Asn	Asn	Asn	Phe	Pro	Asp	Leu	Asn	Thr	Leu	Leu	Trp	Glu
455									460					465
Ala	Glu	Asp	Arg	Gln	Asn	Val	Pro	Arg	Lys	Val	Pro	Asn	His	Tyr
470									475					480
Ile	Ala	Ile	Pro	Glu	Trp	Phe	Leu	Ser	Glu	Asn	Ala	Thr	Val	Ala
485									490					495
Ala	Glu	Thr	Arg	Ala	Val	Ile	Ala	Trp	Met	Glu	Lys	Ile	Pro	Phe

500 505 510

Val	Leu	Gly	Gly	Asn	Leu	Gln	Gly	Gly	Glu	Leu	Val	Val	Ala	Tyr
					515				520				525	
Pro	Tyr	Asp	Leu	Val	Arg	Ser	Pro	Trp	Lys	Thr	Gln	Glu	His	Thr
					530				535				540	
Pro	Thr	Pro	Asp	Asp	His	Val	Phe	Arg	Trp	Leu	Ala	Tyr	Ser	Tyr
					545				550				555	
Ala	Ser	Thr	His	Arg	Leu	Met	Thr	Asp	Ala	Arg	Arg	Arg	Val	Cys
					560				565				570	
His	Thr	Glu	Asp	Phe	Gln	Lys	Glu	Glu	Gly	Thr	Val	Asn	Gly	Ala
					575				580				585	
Ser	Trp	His	Thr	Val	Ala	Gly	Ser	Leu	Asn	Asp	Phe	Ser	Tyr	Leu
					590				595				600	
His	Thr	Asn	Cys	Phe	Glu	Leu	Ser	Ile	Tyr	Val	Gly	Cys	Asp	Lys
					605				610				615	
Tyr	Pro	His	Glu	Ser	Gln	Leu	Pro	Glu	Glu	Trp	Glu	Asn	Asn	Arg
					620				625				630	
Glu	Ser	Leu	Ile	Val	Phe	Met	Glu	Gln	Val	His	Arg	Gly	Ile	Lys
					635				640				645	
Gly	Leu	Val	Arg	Asp	Ser	His	Gly	Lys	Gly	Ile	Pro	Asn	Ala	Ile
					650				655				660	
Ile	Ser	Val	Glu	Gly	Ile	Asn	His	Asp	Ile	Arg	Thr	Ala	Asn	Asp
					665				670				675	
Gly	Asp	Tyr	Trp	Arg	Leu	Leu	Asn	Pro	Gly	Glu	Tyr	Val	Val	Thr
					680				685				690	
Ala	Lys	Ala	Glu	Gly	Phe	Thr	Ala	Ser	Thr	Lys	Asn	Cys	Met	Val
					695				700				705	
Gly	Tyr	Asp	Met	Gly	Ala	Thr	Arg	Cys	Asp	Phe	Thr	Leu	Ser	Lys
					710				715				720	
Thr	Asn	Met	Ala	Arg	Ile	Arg	Glu	Ile	Met	Glu	Lys	Phe	Gly	Lys
					725				730				735	
Gln	Pro	Val	Ser	Leu	Pro	Ala	Arg	Arg	Leu	Lys	Leu	Arg	Gly	Arg
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Lys	Arg	Arg	Gln	Arg	Gly									
					755									

<210> 63

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 63

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ggtacagcag tttacaacaa caacatgtac gtcaacatgt acaacaccgg 1050
gaatattgcc agagttAAC tgaccaccaa cacgattgtc gtgactcaaa 1100
ctctccctaa tgctgcctat aataaccgtc tttcatatgc taatgttgct 1150
tggcaagata ttgactttgc t gttggatgag aatggattgtt gggttattta 1200
ttcaactgaa gccagcactg gtaacatgtt gattgtaaa ctcaatgaca 1250
ccacacttca ggtgctaaac acttggtata ccaagcgtt aaaaaccatct 1300
gtttctaaacg ccttcattgtt atgtgggggtt ctgtatgcca cccgtactat 1350
gaacaccaga acagaagaga tttttacta ttatgcaca aacacaggga 1400
aagaggcga actagacatt gtaatgcata agatgcaggaa aaaagtgcag 1450
agcatttaact ataacccttt tgaccagaaa ctttatgtct ataaacgatgg 1500
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gaaatattt ccaatgact agtccttcatc catgttagcac cactaattct 1950
tccatgcctg gaagaaacctt gggacttagt ttaggtatgt taatatctgg 2000
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aaaa 2854

<210> 67
<211> 510
<212> PRT
<213> Homo sapiens

<400> 67
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20 25 30
Ser Pro Gly Phe Ser Ser Phe Pro Gly Val Asp Ser Ser Ser Ser
35 40 45
Phe Ser Ser Ser Arg Ser Gly Ser Ser Ser Arg Ser Leu
50 55 60
Gly Ser Gly Gly Ser Val Ser Gln Leu Phe Ser Asn Phe Thr Gly
65 70 75
Ser Val Asp Asp Arg Gly Thr Cys Gln Cys Ser Val Ser Leu Pro
80 85 90
Asp Thr Thr Phe Pro Val Asp Arg Val Glu Arg Leu Glu Phe Thr
95 100 105
Ala His Val Leu Ser Gln Lys Phe Glu Lys Glu Leu Ser Lys Val
110 115 120
Arg Glu Tyr Val Gln Leu Ile Ser Val Tyr Glu Lys Lys Leu Leu
125 130 135
Asn Leu Thr Val Arg Ile Asp Ile Met Glu Lys Asp Thr Ile Ser
140 145 150
Tyr Thr Glu Leu Asp Phe Glu Leu Ile Lys Val Glu Val Lys Glu
155 160 165
Met Glu Lys Leu Val Ile Gln Leu Lys Glu Ser Phe Gly Gly Ser
170 175 180
Ser Glu Ile Val Asp Gln Leu Glu Val Glu Ile Arg Asn Met Thr
185 190 195
Leu Leu Val Glu Lys Leu Glu Thr Leu Asp Lys Asn Asn Val Leu
200 205 210

Ala Ile Arg Arg Glu Ile Val Ala Leu Lys Thr Lys Leu Lys Glu
 215 220 225
 Cys Glu Ala Ser Lys Asp Gln Asn Thr Pro Val Val His Pro Pro
 230 235 240
 Pro Thr Pro Gly Ser Cys Gly His Gly Gly Val Val Asn Ile Ser
 245 250 255
 Lys Pro Ser Val Val Gln Leu Asn Trp Arg Gly Phe Ser Tyr Leu
 260 265 270
 Tyr Gly Ala Trp Gly Arg Asp Tyr Ser Pro Gln His Pro Asn Lys
 275 280 285
 Gly Leu Tyr Trp Val Ala Pro Leu Asn Thr Asp Gly Arg Leu Leu
 290 295 300
 Glu Tyr Tyr Arg Leu Tyr Asn Thr Leu Asp Asp Leu Leu Leu Tyr
 305 310 315
 Ile Asn Ala Arg Glu Leu Arg Ile Thr Tyr Gly Gln Gly Ser Gly
 320 325 330
 Thr Ala Val Tyr Asn Asn Asn Met Tyr Val Asn Met Tyr Asn Thr
 335 340 345
 Gly Asn Ile Ala Arg Val Asn Leu Thr Thr Asn Thr Ile Ala Val
 350 355 360
 Thr Gln Thr Leu Pro Asn Ala Ala Tyr Asn Asn Arg Phe Ser Tyr
 365 370 375
 Ala Asn Val Ala Trp Gln Asp Ile Asp Phe Ala Val Asp Glu Asn
 380 385 390
 Gly Leu Trp Val Ile Tyr Ser Thr Glu Ala Ser Thr Gly Asn Met
 395 400 405
 Val Ile Ser Lys Leu Asn Asp Thr Thr Leu Gln Val Leu Asn Thr
 410 415 420
 Trp Tyr Thr Lys Gln Tyr Lys Pro Ser Ala Ser Asn Ala Phe Met
 425 430 435
 Val Cys Gly Val Leu Tyr Ala Thr Arg Thr Met Asn Thr Arg Thr
 440 445 450
 Glu Glu Ile Phe Tyr Tyr Asp Thr Asn Thr Gly Lys Glu Gly
 455 460 465
 Lys Leu Asp Ile Val Met His Lys Met Gln Glu Lys Val Gln Ser
 470 475 480
 Ile Asn Tyr Asn Pro Phe Asp Gln Lys Leu Tyr Val Tyr Asn Asp
 485 490 495
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 500 505 510

<210> 68
 <211> 410
 <212> DNA

055656
1234567890
<213> Homo sapiens
<220>
<221> unsure
<222> 206, 217, 387
<223> unknown base

<400> 68
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ggtgaacatc agcaaaccgt ctgtggttca gctcaactgg agagggttt 150
cttatctata tggtgcttgg gtagggatt actctccccaa 200
aaaggatgtt attgggnggc gccattgaat acagatggga gactgttgg 250
gtattataga ctgtacaacc cactggatga tttgtatattg tatataaatgg 300
ctcgagagggtt gcggttaccatggccaaatggatgttac agcagtttac 350
aacaaacaaca tggtaacatc catgtacaac accgggnata ttgccagagt 400
taacctgacc 410

<210> 69
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 69
agctgtggtc atgggttgtt ggtt 24

<210> 70
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
ctaccttggc catagggtat ccgc 24

<210> 71
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 71
catcagcaaa ccgtctgtgg ttcaagctcaa ctggagaggg tt 42

<210> 72
<211> 3127
<212> DNA
<213> Homo sapiens

卷之三

<400> 72
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ccgtgttgc tatgccatgtc ctgtccatgt ggaaacaact ccactgtaac 200
tagattgtatc tatgcacttt tcttgttgc tggagatgtt gtatgttgc 250
taatgttgc accaggaatg gaagaacaac tgaataagat tcctggattt 300
tgtgagaatg agaaagggtgt tgcccttgtaa aacattttgg ttggctataa 350
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cctctgcgtt ggtgttgc taaatgttatc actgccccaa atccaagaat 850
cacaaccaatg atctgggttgc ttacatcgatc cgtatccatgc 900
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<213> Homo sapiens

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35 40 45
Leu Leu Val Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly
50 55 60
Met Glu Glu Gln Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu
65 70 75
Lys Gly Val Val Pro Cys Asn Ile Leu Val Gly Tyr Lys Ala Val
80 85 90
Tyr Arg Leu Cys Phe Gly Leu Ala Met Phe Tyr Leu Leu Leu Ser
95 100 105
Leu Leu Met Ile Lys Val Lys Ser Ser Asp Pro Arg Ala Ala
110 115 120
Val His Asn Gly Phe Trp Phe Phe Lys Phe Ala Ala Ala Ile Ala
125 130 135
Ile Ile Ile Gly Ala Phe Phe Ile Pro Glu Gly Thr Phe Thr Thr
140 145 150
Val Trp Phe Tyr Val Gly Met Ala Gly Ala Phe Cys Phe Ile Leu
155 160 165
Ile Gln Leu Val Leu Leu Ile Asp Phe Ala His Ser Trp Asn Glu
170 175 180
Ser Trp Val Glu Lys Met Glu Glu Gly Asn Ser Arg Cys Trp Tyr
185 190 195
Ala Ala Leu Leu Ser Ala Thr Ala Leu Asn Tyr Leu Leu Ser Leu
200 205 210
Val Ala Ile Val Leu Phe Phe Val Tyr Tyr Thr His Pro Ala Ser
215 220 225
Cys Ser Glu Asn Lys Ala Phe Ile Ser Val Asn Met Leu Leu Cys
230 235 240
Val Gly Ala Ser Val Met Ser Ile Leu Pro Lys Ile Gln Glu Ser
245 250 255
Gln Pro Arg Ser Gly Leu Leu Gln Ser Ser Val Ile Thr Val Tyr
260 265 270
Thr Met Tyr Leu Thr Trp Ser Ala Met Thr Asn Glu Pro Glu Thr
275 280 285

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Asn Cys Asn Pro Ser Leu Leu Ser Ile Ile Gly Tyr Asn Thr Thr
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Ser Thr Val Pro Lys Glu Gly Gln Ser Val Gln Trp Trp His Ala
305 310 315

Gln Gly Ile Ile Gly Leu Ile Leu Phe Leu Leu Cys Val Phe Tyr
320 325 330

Ser Ser Ile Arg Thr Ser Asn Asn Ser Gln Val Asn Lys Leu Thr
335 340 345

Leu Thr Ser Asp Glu Ser Thr Leu Ile Glu Asp Gly Gly Ala Arg
350 355 360

Ser Asp Gly Ser Leu Glu Asp Gly Asp Asp Val His Arg Ala Val
365 370 375

Asp Asn Glu Arg Asp Gly Val Thr Tyr Ser Tyr Ser Phe Phe His
380 385 390

Phe Met Leu Phe Leu Ala Ser Leu Tyr Ile Met Met Thr Leu Thr
395 400 405

Asn Trp Ser Arg Tyr Glu Pro Ser Arg Glu Met Lys Ser Gln Trp
410 415 420

Thr Ala Val Trp Val Lys Ile Ser Ser Trp Ile Gly Ile Val
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<213> Homo sapiens

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<222> 48, 163
<223> unknown base

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tgctgcgca attgcaatta ttattgggc 480
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<211> 438
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 65, 92, 121, 142, 154, 170, 293, 315, 323
<223> unknown base

<400> 75
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tggagaaca actgaataag attcctggat tttgtgagaa tgaaaaagg 250
gttgtccctt gtaacatccc gggtggctat aaagctgtat atngttgtt 300
ctttgggtttt gctangttct atnttcttct ctctttacta atgatcaa 350
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tttaaattttt ctgcagcaat tgcaattttt atttgggc 438

<210> 76
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 48
<223> unknown base

<400> 76
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acaactcca ctgtaaacttgc attgtatcttgc acacttttgc tgctgttgc 200
agtatgtgttgc gcttgcgttgc tggtgatacc aggaatggaa gaacaacttgc 250
ataagattcc tggattttgc gagaatggaa aagggtttgttgc cccttgcac 300
attttgggttgc gctataaagg tgcgtatgttgc tggttgcata 350
gttctatctt ctctctctt tactaatgtt caaaatgttgc agtagcgttgc 400
atcccttaggc tgcaatgttgc acatggattttgc gtttctttaa atttgttgc 450

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 81
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
gagcatgccca ccactggact gac 23

<210> 82
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
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<212> DNA
<213> Homo sapiens

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aatcccacat ctgtttcaac tctccggccga gggcgagccg gagcgagagt 500
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<211> 867
<212> PRT
<213> Homo sapiens

<400> 84
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Ile Ile Leu Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser
50 55 60
Met Gln Val Met Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly
65 70 75
Ala His Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys Cys Pro
80 85 90
Ser Arg Ser Ser Ile Leu Thr Gly Lys Tyr Val His Asn His Asn
95 100 105
Thr Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala
110 115 120
Gln His Glu Ser Arg Thr Phe Ala Val Tyr Leu Asn Ser Thr Gly
125 130 135
Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly
140 145 150
Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp Val Gly Leu Leu Lys
155 160 165
Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg Asn Gly Val Lys
170 175 180
Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu Thr Asp Leu
185 190 195
Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys Lys Met
200 205 210
Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala Pro
215 220 225
His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro
230 235 240
Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn
245 250 255

Pro	Asp	Lys	His	Trp	Ile	Met	Arg	Tyr	Thr	Gly	Pro	Met	Lys	Pro
				260						265				270
Ile	His	Met	Glu	Phe	Thr	Asn	Met	Leu	Gln	Arg	Lys	Arg	Leu	Gln
				275					280					285
Thr	Leu	Met	Ser	Val	Asp	Asp	Ser	Met	Glu	Thr	Ile	Tyr	Asn	Met
				290				295					300	
Leu	Val	Glu	Thr	Gly	Glu	Leu	Asp	Asn	Thr	Tyr	Ile	Val	Tyr	Thr
				305				310					315	
Ala	Asp	His	Gly	Tyr	His	Ile	Gly	Gln	Phe	Gly	Leu	Val	Lys	Gly
				320				325					330	
Lys	Ser	Met	Pro	Tyr	Glu	Phe	Asp	Ile	Arg	Val	Pro	Phe	Tyr	Val
				335				340					345	
Arg	Gly	Pro	Asn	Val	Glu	Ala	Gly	Cys	Leu	Asn	Pro	His	Ile	Val
				350				355					360	
Leu	Asn	Ile	Asp	Leu	Ala	Pro	Thr	Ile	Leu	Asp	Ile	Ala	Gly	Leu
				365				370					375	
Asp	Ile	Pro	Ala	Asp	Met	Asp	Gly	Lys	Ser	Ile	Leu	Lys	Leu	Leu
				380				385					390	
Asp	Thr	Glu	Arg	Pro	Val	Asn	Arg	Phe	His	Leu	Lys	Lys	Lys	Met
				395				400					405	
Arg	Val	Trp	Arg	Asp	Ser	Phe	Leu	Val	Glu	Arg	Gly	Lys	Leu	Leu
				410				415					420	
His	Lys	Arg	Asp	Asn	Asp	Lys	Val	Asp	Ala	Gln	Glu	Glu	Asn	Phe
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Leu	Pro	Lys	Tyr	Gln	Arg	Val	Lys	Asp	Leu	Cys	Gln	Arg	Ala	Glu
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Glu	Asp	Ala	Thr	Gly	Lys	Leu	Lys	Leu	His	Lys	Cys	Lys	Gly	Pro
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Met	Arg	Leu	Gly	Gly	Ser	Arg	Ala	Leu	Ser	Asn	Leu	Val	Pro	Lys
				485				490					495	
Tyr	Tyr	Gly	Gln	Gly	Ser	Glu	Ala	Cys	Thr	Cys	Asp	Ser	Gly	Asp
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Tyr	Lys	Leu	Ser	Leu	Ala	Gly	Arg	Arg	Lys	Lys	Leu	Phe	Lys	Lys
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Ala	Ile	Glu	Val	Asp	Gly	Arg	Val	Tyr	His	Val	Gly	Leu	Gly	Asp
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Ala	Ala	Gln	Pro	Arg	Asn	Leu	Thr	Lys	Arg	His	Trp	Pro	Gly	Ala
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Pro Glu Asp Gln Asp Asp Lys Asp Gly Gly Asp Phe Ser Gly Thr
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 Gly Gly Leu Pro Asp Tyr Ser Ala Ala Asn Pro Ile Lys Val Thr
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 His Arg Cys Tyr Ile Leu Glu Asn Asp Thr Val Gln Cys Asp Leu
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 Gln Thr Ala Pro Phe Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr
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<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe
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<210> 86
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ggccagctat ctccgcag 18

<210> 87
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<400> 87
aaggccctgc aagagaag 18

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<400> 88
cactgggaca actgtggg 18

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<400> 89
cagaggcaac gtggagag 18

<210> 90
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<212> DNA
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<220>
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aagtattgtc atacagtgtt c 21

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aaaaaaaaaa aaaaaaaaaa a 971

<210> 95
<211> 115
<212> PRT
<213> Homo sapiens

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Gly Ala Ala Val Ala Val Leu Leu Leu Leu Leu Ala Thr
20 25 30
Cys Leu Phe His Gly Arg Gln Asp Cys Asp Val Glu Arg Asn Arg
35 40 45
Thr Ala Ala Gly Gly Asn Arg Val Arg Arg Ala Gln Pro Trp Pro
50 55 60
Phe Arg Arg Arg Gly His Leu Gly Ile Phe His His His Arg His
65 70 75
Pro Gly His Val Ser His Val Pro Asn Val Gly Leu His His His
80 85 90
His His Pro Arg His Thr Pro His His Leu His His His His His
95 100 105
Pro His Arg His His Pro Arg His Ala Arg
110 115

<210> 96
<211> 1312
<212> DNA
<213> Homo sapiens

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aagtgagtgc tgggtcaccc cccatccgca acgtcactgt ggcctacaag 200
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<210> 97
<211> 313
<212> PRT
<213> Homo sapiens

<400> 97
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35 40 45
Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr
50 55 60
Gly Arg Leu Phe Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg
65 70 75

Ser Ile Ala Val Tyr Tyr Asp Asn Pro His Met Val Pro Pro Asp
80 85 90

Lys Cys Arg Cys Ala Val Gly Ser Ile Leu Ser Glu Gly Glu Glu
95 100 105

Ser Pro Ser Pro Glu Leu Ile Asp Leu Tyr Gln Lys Phe Gly Phe
110 115 120

Lys Val Phe Ser Phe Pro Ala Pro Ser His Val Val Thr Ala Thr
125 130 135

Phe Pro Tyr Thr Thr Ile Leu Ser Ile Trp Leu Ala Thr Arg Arg
140 145 150

Val His Pro Ala Leu Asp Thr Tyr Ile Lys Glu Arg Lys Leu Cys
155 160 165

Ala Tyr Pro Arg Leu Glu Ile Tyr Gln Glu Asp Gln Ile His Phe
170 175 180

Met Cys Pro Leu Ala Arg Gln Gly Asp Phe Tyr Val Pro Glu Met
185 190 195

Lys Glu Thr Glu Trp Lys Trp Arg Gly Leu Val Glu Ala Ile Asp
200 205 210

Thr Gln Val Asp Gly Thr Gly Ala Asp Thr Met Ser Asp Thr Ser
215 220 225

Ser Val Ser Leu Glu Val Ser Pro Gly Ser Arg Glu Thr Ser Ala
230 235 240

Ala Thr Leu Ser Pro Gly Ala Ser Ser Arg Gly Trp Asp Asp Gly
245 250 255

Asp Thr Arg Ser Glu His Ser Tyr Ser Glu Ser Gly Ala Ser Gly
260 265 270

Ser Ser Phe Glu Glu Leu Asp Leu Glu Gly Glu Gly Pro Leu Gly
275 280 285

Glu Ser Arg Leu Asp Pro Gly Thr Glu Pro Leu Gly Thr Thr Lys
290 295 300

Trp Leu Trp Glu Pro Thr Ala Pro Glu Lys Gly Lys Glu
305 310

<210> 98
<211> 725
<212> DNA
<213> Homo sapiens

<400> 98
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ccccggctcc ctgcccccgcc cccagtcatg accctgcgcc cctcaactct 100
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ctgaggctgg gctcgaaacc gaaagtccccg tccggaccc ccaagtggag 200
accctgggtgg agcccccaaga accatgtgcg gagcccgctg cttttggaga 250

cacgcttcac atacactaca cggaaagctt ggttagatgga cgtattattg 300
acacccctt gaccagagc cctctggta tagaacttgg ccaaaagcag 350
gtgattccag gtctggagca gagtcttctc gacatgtgtg tgggagagaa 400
gcgaaggcca atcattcctt ctcaacttggc ctatggaaaa cggggatttc 450
caccatctgt cccagcggat gcagtgggtc agtatgacgt ggagctgatt 500
gcactaatcc gagccaacta ctggctaaag ctggtaagg gcatttgcc 550
tctggtagg atggccatgg tgccagccct cctgggcctc attgggtatc 600
acctatacag aaaggccaaat agacccaaag tctccaaaaa gaagctcaag 650
gaagagaaaac gaaacaagag caaaaagaaa taataaataa taaattttaa 700
aaaacttaaa aaaaaaaaaa aaaaa 725

<210> 99
<211> 201
<212> PRT
<213> Homo sapiens

<400> 99
Met Thr Leu Arg Pro Ser Leu Leu Pro Leu His Leu Leu Leu
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Leu Leu Leu Ser Ala Ala Val Cys Arg Ala Glu Ala Gly Leu Glu
20 25 30
Thr Glu Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu
35 40 45
Pro Pro Glu Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu
50 55 60
His Ile His Tyr Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp
65 70 .75
Thr Ser Leu Thr Arg Asp Pro Leu Val Ile Glu Leu Gly Gln Lys
80 85 90
Gln Val Ile Pro Gly Leu Glu Gln Ser Leu Leu Asp Met Cys Val
95 100 105
Gly Glu Lys Arg Arg Ala Ile Ile Pro Ser His Leu Ala Tyr Gly
110 115 120
Lys Arg Gly Phe Pro Pro Ser Val Pro Ala Asp Ala Val Val Gln
125 130 135
Tyr Asp Val Glu Leu Ile Ala Leu Ile Arg Ala Asn Tyr Trp Leu
140 145 150
Lys Leu Val Lys Gly Ile Leu Pro Leu Val Gly Met Ala Met Val
155 160 165
Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu Tyr Arg Lys Ala
170 175 180
Asn Arg Pro Lys Val Ser Lys Lys Lys Leu Lys Glu Glu Lys Arg

15816060

185

190

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Asn Lys Ser Lys Lys Lys
200

<210> 100
<211> 705
<212> DNA
<213> Homo sapiens

<400> 100
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gaggctggcc tcgaaaccga aagtcccgtc cgaccctcc aagtggagac 200
cctggtgag cccccagaac catgtgcoga gcccgtgct tttggagaca 250
cgcttcacat acactacacg ggaagctgg tagatggacg tattattgac 300
acctccctga ccagagaccc tctgggtata gaacttggcc aaaaggcagg 350
gattccaggct ctggaggcaga gtcttctca catgtgtgt ggagagaagc 400
gaagggcaat catttctt cacttggcct atggaaaacg gggatttcca 450
ccatctgtcc cagcggatgc agtggtgca gatgacgtgg agctgattgc 500
actaatccga gccaactact ggctaaaggct ggtgaagggc attttgcctc 550
tggtagggat ggccatggtg ccaccctcc gggcctcatt ggtatcacc 600
tatacagaaa ggccaataga cccaaaggct cccaaaagaa gctcaaggaa 650
gagaaacgaa acaagagcaa aaagaaataa taaaataaa attttaaaaa 700
actta 705

<210> 101
<211> 543
<212> DNA
<213> Homo sapiens

<400> 101
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accctctggat tatagaactt ggccaaaacg aggtgattcc aggtctggag 200
cagagtcttc tgcacatgtg tgtggagag aagcgaaggg caatcattcc 250
ttctctacttgc ctatggaa aacggggatt tccaccatct gtcccagcgg 300
atgcagtggtt gcagttatgac gtggagctgat ttgcactaat ccgagccaa 350
tactggctaa agctggtaa gggcattttgc cctctggtag ggatggccat 400

gggccagcc ctctggcc tcattggta tacccatac agaaaggcca 450
atagacccaa agtctccaaa aagaagtc aggaagagaa acgaaacaag 500
agaaaaaga ataataaat aataaattt aaaaaactta aaa 543

<210> 102
<211> 1316
<212> DNA
<213> Homo sapiens

<400> 102
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gagggtctga gatgctcaga atgcattgtc tggtggggaaa agcgcataac 200
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<210> 103

<211> 157

<212> PRT

<213> Homo sapiens

<400> 103

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Trp Gly Glu Lys Arg Asn Thr Ile Ala Ser Ile Ala Ala Gly Val

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Leu Phe Phe Thr Gly Trp Trp Ile Ile Ile Asp Ala Ala Val Ile

35

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45

Tyr Pro Thr Met Lys Asp Phe Asn His Ser Tyr His Ala Cys Gly

50

55

60

Val Ile Ala Thr Ile Ala Phe Leu Met Ile Asn Ala Val Ser Asn

65

70

75

Gly Gln Val Arg Gly Asp Ser Tyr Ser Glu Gly Cys Leu Gly Gln

80

85

90

Thr Gly Ala Arg Ile Trp Leu Phe Val Gly Phe Met Leu Ala Phe

95

100

105

Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Gly Tyr Val

110

115

120

Ala Lys Glu Lys Asp Ile Val Tyr Pro Gly Ile Ala Val Phe Phe

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Gln Asn Ala Phe Ile Phe Phe Gly Gly Leu Val Phe Lys Phe Gly

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Arg Thr Glu Asp Leu Trp Gln

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<210> 104

<211> 545

<212> DNA

<213> Homo sapiens

<400> 104

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<210> 105
<211> 490
<212> DNA
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<220>
<221> unsure
<222> 31, 39, 108, 145, 179, 219, 412, 479
<223> unknown base

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<210> 106
<211> 466
<212> DNA
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<220>
<221> unsure
<222> 26, 38, 81, 115, 207, 329, 380, 446, 449
<223> unknown base

<400> 106
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tg 552

<210> 109
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 109
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<210> 110
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<220>
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<400> 110
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<210> 111
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<220>
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<210> 112
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<210> 113
<211> 610
<212> PRT
<213> Homo sapiens

<400> 113
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35 40 45
Thr Asp Lys Glu Ala Arg Lys Lys Val Leu Lys Gln Ala Phe Ser
50 55 60
Ala Asn Gln Val Pro Glu Lys Leu Asp Val Val Val Ile Gly Ser
65 70 75
Gly Phe Gly Gly Leu Ala Ala Ala Ala Ile Leu Ala Lys Ala Gly
80 85 90
Lys Arg Val Leu Val Leu Glu Gln His Thr Lys Ala Gly Gly Cys
95 100 105

Cys His Thr Phe Gly Lys Asn Gly Leu Glu Phe Asp Thr Gly Ile
 110 115 120
 His Tyr Ile Gly Arg Met Glu Glu Gly Ser Ile Gly Arg Phe Ile
 125 130 135
 Leu Asp Gln Ile Thr Glu Gly Gln Leu Asp Trp Ala Pro Leu Ser
 140 145 150
 Ser Pro Phe Asp Ile Met Val Leu Glu Gly Pro Asn Gly Arg Lys
 155 160 165
 Glu Tyr Pro Met Tyr Ser Gly Glu Lys Ala Tyr Ile Gln Gly Leu
 170 175 180
 Lys Glu Lys Phe Pro Gln Glu Glu Ala Ile Ile Asp Lys Tyr Ile
 185 190 195
 Lys Leu Val Lys Val Val Ser Ser Gly Ala Pro His Ala Ile Leu
 200 205 210
 Leu Lys Phe Leu Pro Leu Pro Val Val Gln Leu Leu Asp Arg Cys
 215 220 225
 Gly Leu Leu Thr Arg Phe Ser Pro Phe Leu Gln Ala Ser Thr Gln
 230 235 240
 Ser Leu Ala Glu Val Leu Gln Gln Leu Gly Ala Ser Ser Glu Leu
 245 250 255
 Gln Ala Val Leu Ser Tyr Ile Phe Pro Thr Tyr Gly Val Thr Pro
 260 265 270
 Asn His Ser Ala Phe Ser Met His Ala Leu Leu Val Asn His Tyr
 275 280 285
 Met Lys Gly Gly Phe Tyr Pro Arg Gly Gly Ser Ser Glu Ile Ala
 290 295 300
 Phe His Thr Ile Pro Val Ile Gln Arg Ala Gly Gly Ala Val Leu
 305 310 315
 Thr Lys Ala Thr Val Gln Ser Val Leu Leu Asp Ser Ala Gly Lys
 320 325 330
 Ala Cys Gly Val Ser Val Lys Lys Gly His Glu Leu Val Asn Ile
 335 340 345
 Tyr Cys Pro Ile Val Val Ser Asn Ala Gly Leu Phe Asn Thr Tyr
 350 355 360
 Glu His Leu Leu Pro Gly Asn Ala Arg Cys Leu Pro Gly Val Lys
 365 370 375
 Gln Gln Leu Gly Thr Val Arg Pro Gly Leu Gly Met Thr Ser Val
 380 385 390
 Phe Ile Cys Leu Arg Gly Thr Lys Glu Asp Leu His Leu Pro Ser
 395 400 405
 Thr Asn Tyr Tyr Val Tyr Tyr Asp Thr Asp Met Asp Gln Ala Met
 410 415 420

Glu Arg Tyr Val Ser Met Pro Arg Glu Glu Ala Ala Glu His Ile
425 430 435
Pro Leu Leu Phe Phe Ala Phe Pro Ser Ala Lys Asp Pro Thr Trp
440 445 450
Glu Asp Arg Phe Pro Gly Arg Ser Thr Met Ile Met Leu Ile Pro
455 460 465
Thr Ala Tyr Glu Trp Phe Glu Glu Trp Gln Ala Glu Leu Lys Gly
470 475 480
Lys Arg Gly Ser Asp Tyr Glu Thr Phe Lys Asn Ser Phe Val Glu
485 490 495
Ala Ser Met Ser Val Val Leu Lys Leu Phe Pro Gln Leu Glu Gly
500 505 510
Lys Val Glu Ser Val Thr Ala Gly Ser Pro Leu Thr Asn Gln Phe
515 520 525
Tyr Leu Ala Ala Pro Arg Gly Ala Cys Tyr Gly Ala Asp His Asp
530 535 540
Leu Gly Arg Leu His Pro Cys Val Met Ala Ser Leu Arg Ala Gln
545 550 555
Ser Pro Ile Pro Asn Leu Tyr Leu Thr Gly Gln Asp Ile Phe Thr
560 565 570
Cys Gly Leu Val Gly Ala Leu Gln Gly Ala Leu Leu Cys Ser Ser
575 580 585
Ala Ile Leu Lys Arg Asn Leu Tyr Ser Asp Leu Lys Asn Leu Asp
590 595 600
Ser Arg Ile Arg Ala Gln Lys Lys Lys Asn
605 610

<210> 114
<211> 1701
<212> DNA
<213> Homo sapiens

<400> 114
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cgtccctcgga tgaagaaggc agccaggatg aatccttaga ttccaagact 200
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atgtgttgtt caaatatttt ttgattcaga agaatctgaa ttggatcc 300
ctattcaaga agaggaagac agcctcaaga gccaagaggg ggaaagtgtc 350
acagaagata tcaagttttt agagtctcca aatccagaaa acaaggacta 400
tgaagagcca aagaaaatgc gaaaaaccgc ttgaccgc attgaaggca 450

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tatgtatcatgtatcaga tggggggaa gatggcagac tgggtgtgc 550
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aatatccagg cagcgagaga gatgttttag aagctgactg aggaaggctc 850
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aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1700

a 1701

<210> 115

<211> 301

<212> PRT

<213> Homo sapiens

<400> 115

Met Arg Val Arg Ile Gly Leu Thr Leu Leu Leu Cys Ala Val Leu

1

Leu Ser I

20 25 30

100

HOMO SAPIENS

Glu	Ser	Leu	Asp	Ser	Lys	Thr	Thr	Leu	Thr	Ser	Asp	Glu	Ser	Val
35														45
Lys	Asp	His	Thr	Thr	Ala	Gly	Arg	Val	Val	Ala	Gly	Gln	Ile	Phe
50														60
Leu	Asp	Ser	Glu	Glu	Ser	Glu	Leu	Glu	Ser	Ser	Ile	Gln	Glu	Glu
														75
Glu	Asp	Ser	Leu	Lys	Ser	Gln	Glu	Gly	Glu	Ser	Val	Thr	Glu	Asp
				80							85			90
Ile	Ser	Phe	Leu	Glu	Ser	Pro	Asn	Pro	Glu	Asn	Lys	Asp	Tyr	Glu
				95							100			105
Glu	Pro	Lys	Lys	Val	Arg	Lys	Pro	Ala	Leu	Thr	Ala	Ile	Glu	Gly
				110						115				120
Thr	Ala	His	Gly	Glu	Pro	Cys	His	Phe	Pro	Phe	Leu	Phe	Leu	Asp
				125						130				135
Lys	Glu	Tyr	Asp	Glu	Cys	Thr	Ser	Asp	Gly	Arg	Glu	Asp	Gly	Arg
				140						145				150
Leu	Trp	Cys	Ala	Thr	Thr	Tyr	Asp	Tyr	Lys	Ala	Asp	Glu	Lys	Trp
				155					160					165
Gly	Phe	Cys	Glu	Thr	Glu	Glu	Ala	Ala	Lys	Arg	Arg	Gln	Met	
				170					175					180
Gln	Glu	Ala	Glu	Met	Met	Tyr	Gln	Thr	Gly	Met	Lys	Ile	Leu	Asn
				185					190					195
Gly	Ser	Asn	Lys	Lys	Ser	Gln	Lys	Arg	Glu	Ala	Tyr	Arg	Tyr	Leu
				200					205					210
Gln	Lys	Ala	Ala	Ser	Met	Asn	His	Thr	Lys	Ala	Leu	Glu	Arg	Val
				215					220					225
Ser	Tyr	Ala	Leu	Leu	Phe	Gly	Asp	Tyr	Leu	Pro	Gln	Asn	Ile	Gln
				230					235					240
Ala	Ala	Arg	Glu	Met	Phe	Glu	Lys	Leu	Thr	Glu	Glu	Gly	Ser	Pro
				245					250					255
Lys	Gly	Gln	Thr	Ala	Leu	Gly	Phe	Leu	Tyr	Ala	Ser	Gly	Leu	Gly
				260					265					270
Val	Asn	Ser	Ser	Gln	Ala	Lys	Ala	Leu	Val	Tyr	Tyr	Thr	Phe	Gly
				275					280					285
Ala	Leu	Gly	Gly	Asn	Leu	Ile	Ala	His	Met	Val	Leu	Val	Ser	Arg
				290					295					300

Leu

<210> 116
<211> 584
<212> DNA
<213> Homo sapiens

<400> 116

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agctggatgc actgtcggtc ttcccagggc aagtggctca acttcctcgc 200
acgctcagcc cccagcacgt caccatcagg gactacggtg tgtcctggta 250
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aaaatgggtt aataatattc aacatgtcaa caac 584

<210> 117

<211> 123

<212> PRT

<213> Homo sapiens

<400> 117

Met	Ala	Cys	Arg	Cys	Leu	Ser	Phe	Leu	Leu	Met	Gly	Thr	Phe	Leu
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Ser	Val	Ser	Gln	Thr	Val	Leu	Ala	Gln	Leu	Asp	Ala	Leu	Leu	Val
				20					25					30

Phe	Pro	Gly	Gln	Val	Ala	Gln	Leu	Ser	Cys	Thr	Leu	Ser	Pro	Gln
				35					40					45

His	Val	Thr	Ile	Arg	Asp	Tyr	Gly	Val	Ser	Trp	Tyr	Gln	Gln	Arg
				50					55					60

Ala	Gly	Ser	Ala	Pro	Arg	Tyr	Leu	Leu	Tyr	Tyr	Arg	Ser	Glu	Glu
				65					70					75

Asp	His	His	Arg	Pro	Ala	Asp	Ile	Pro	Asp	Arg	Phe	Ser	Ala	Ala
				80					85					90

Lys	Asp	Glu	Ala	His	Asn	Ala	Cys	Val	Leu	Thr	Ile	Ser	Pro	Val
				95					100					105

Gln	Pro	Glu	Asp	Asp	Ala	Asp	Tyr	Tyr	Cys	Ser	Val	Gly	Tyr	Gly
				110					115					120

Phe Ser Pro

<210> 118

<211> 3402

<212> DNA

<213> Homo sapiens

<400> 118

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aa 3402

<210> 119

<211> 504

<212> PRT

<213> Homo sapiens

<400> 119

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Leu	Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys
	20							25					30
Met	Ala	Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly
		35					40				45		
Thr	Val	Arg	Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Leu
		50						55				60	
Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp
			65					70				75	
Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val
			80						85				90
Arg	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly
		95						100				105	
Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Val	Val	Leu	Asp	Asp
		110						115				120	
Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly
		125						130				135	
Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe
		140							145				150
Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
		155						160				165	
Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg
		170							175				180
Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	Arg	Pro
			185						190				195
Ala	Ala	Glu	Pro	Arg	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn
			200					205				210	
Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser
			215					220				225	
Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
			230						235				240

Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
245 250 255

Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val
260 265 270

Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu
275 280 285

Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly
290 295 300

Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro
305 310 315

Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln
320 325 330

Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly
335 340 345

Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys
350 355 360

Pro Pro Gly Pro Pro Val Ala Ser Ser Ser Ser Ala Thr Ser Leu
365 370 375

Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile
380 385 390

Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro
395 400 405

Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His Arg Pro Pro
410 415 420

Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu
425 430 435

Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His
440 445 450

Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val
455 460 465

Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr
470 475 480

His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys
485 490 495

Val His Gln His Ile His Tyr Gln Cys
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<210> 120

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

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<210> 121
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 121
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<210> 122
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 122
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<210> 123
<211> 4420
<212> DNA
<213> Homo sapiens

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gcctgggtgt tctcttctct ggtctggaa gtcacatctg tgttggggag 200
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<211> 1184

<212> PRT

<213> Homo sapiens

<400> 124

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Ala	Ile	Arg	Phe	Tyr	Tyr	Gly	Asp	Arg	Val	Cys	Ala	Arg	Pro	Leu
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Ser	Cys	Gln	Arg	Cys	Thr	Glu	Thr	Arg	Ser	Ile	Val	Arg	Gly	Arg
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Val	Ser	Ala	Ala	Asp	Asn	Gly	Glu	Pro	Met	Arg	Phe	Gly	His	Val
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 680 685 690
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<212> DNA
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ప్రాణికాల విషయాలు

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35 40 45
Asp Tyr Met Ala Cys Gln Pro Glu Ser Thr Asp Met Thr Lys Tyr
50 55 60
Leu Lys Val Lys Leu Asp Pro Pro Asp Ile Thr Cys Gly Asp Pro
65 70 75
Pro Glu Thr Phe Cys Ala Met Gly Asn Pro Tyr Met Cys Asn Asn
80 85 90
Glu Cys Asp Ala Ser Thr Pro Glu Leu Ala His Pro Pro Glu Leu
95 100 105
Met Phe Asp Phe Glu Gly Arg His Pro Ser Thr Phe Trp Gln Ser
110 115 120
Ala Thr Trp Lys Glu Tyr Pro Lys Pro Leu Gln Val Asn Ile Thr

Tyr Ile Val Phe Ser Gly Asn Pro Lys Cys

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Thr Phe Glu Ser Gly Arg Pro Asp Gln Met Ile Leu Glu Lys Ser			
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Leu Asp Tyr Gly Arg Thr Trp Gln Pro Tyr Gln Tyr Tyr Ala Thr			
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Asp Cys Leu Asp Ala Phe His Met Asp Pro Lys Ser Val Lys Asp			
185	190	195	
Leu Ser Gln His Thr Val Leu Glu Ile Ile Cys Thr Glu Glu Tyr			
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Ser Thr Gly Tyr Thr Thr Asn Ser Lys Ile Ile His Phe Glu Ile			
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Ala Ser Leu Tyr Gly Gln Leu Asp Thr Thr Lys Lys Leu Arg Asp			
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Phe Phe Thr Val Thr Asp Leu Arg Ile Arg Leu Leu Arg Pro Ala			
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Val Gly Glu Ile Phe Val Asp Glu Leu His Leu Ala Arg Tyr Phe			
275	280	285	
Tyr Ala Ile Ser Asp Ile Lys Val Arg Gly Arg Cys Lys Cys Asn			
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Leu His Ala Thr Val Cys Val Tyr Asp Asn Ser Lys Leu Thr Cys			
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Glu Cys Glu His Asn Thr Thr Gly Pro Asp Cys Gly Lys Cys Lys			
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Lys Asn Tyr Gln Gly Arg Pro Trp Ser Pro Gly Ser Tyr Leu Pro			
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Ile Gly Thr Asn Val Cys Asp Asn Glu Leu Leu His Cys Gln Asn			
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395	400	405	
Ser Cys Gly Ser Asp Ser Gly Gln Gly Ala Pro Pro His Gly Thr			
410	415	420	
Pro Ala Leu Leu Leu Leu Thr Thr Leu Leu Gly Thr Ala Ser Pro			
425	430	435	
Leu Val Phe			

1000 900 800 700 600 500

<210> 130
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 130
tcgattatgg acgaacatgg cagc 24

<210> 131
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 131
ttctgagatc cctcatcctc 20

<210> 132
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 132
aggttcaggc acagcaagt tggg 24

<210> 133
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 133
tttgctggac ctccgctacg gaattggctt ccctctacgg acagctggat 50

<210> 134
<211> 1493
<212> DNA
<213> Homo sapiens

<400> 134
cccacgcgtc cgggtgacct gggccgagcc ctcccggtcg gctaagattg 50
ctgaggaggc ggcgggttagc tggcaggcgc cgacttccga aggccgcgt 100
ccgggcgagg tgtccctatc acttctcttg tggaccatgt ccgtgatctt 150
ttttgcctgc gtggtaacggg taaggatgg actgccccctc tcagcctcta 200
ctgatttttta ccacacccaa gattttttg aatggaggag acggctcaag 250
agttagct tgcgactggc ccagtatcca ggtcgagggtt ctgcagaagg 300

tttgtacttt agtatacatt tttttttttt cggggacgtg gctgcattgg 350
ctatctgctc ctgccagtgt ccagcagcca tggcattctg cttccctggag 400
accctgttgtt gggatttcac agcttcctat gacactacct gatggcct 450
agcctccagg ccatacgctt ttcttgagtt tgacagcatc attcagaag 500
tgaagtggca ttttaactat gtaagttcct ctcagatgg gtcagctt 550
aaaaaaattc aggaggagct caagttgcag cttccagcgg ttctcactct 600
ggaggacaca gatgtggcaa atgggtgtat gaatggtcac acaccgtgc 650
acttggagcc tgctcctaatttccaaatgg aaccagtgc acccctgggt 700
atccctccccc tcattctcaa catcatgtgt gtcgcctga atctcatcg 750
aggagttcac cttgcagaaatccataa ggatccaagg agctggttct 800
gctgggtggca ccaaaccatcg tgagccagcc acccctgacc caaatgagga 850
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gcataaaaata ctgaggctga tttagtcagg gcaaaaccat ttactttaca 1250
tattcggtttt caatacttcg ttttagtcagg ttttagtcagg gcaaaaccat ttactttaca 1300
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tcagtagtac aacccatggat tttttttttt tttttttttt tttttttttt 1400
tttatatccctt atgtataat taaaatggatggt ggcttcagaa atggcagaat 1450
aaatctaaag tgtttattaa aaaaaaaaaa aaaaaaaaaa aag 1493

<210> 135

<211> 228

<212> PRT

<213> Homo sapiens

<400> 135

Met	Ser	Val	Ile	Phe	Ala	Cys	Val	Val	Arg	Val	Arg	Asp	Gly	
1				5				10					15	
Leu	Pro	Leu	Ser	Ala	Ser	Thr	Asp	Phe	Tyr	His	Thr	Gln	Asp	Phe
				20					25					30
Leu	Glu	Trp	Arg	Arg	Arg	Leu	Lys	Ser	Leu	Ala	Leu	Arg	Leu	Ala
				35					40					45

Gln Tyr Pro Gly Arg Gly Ser Ala Glu Gly Cys Asp Phe Ser Ile
50 55 60
His Phe Ser Ser Phe Gly Asp Val Ala Cys Met Ala Ile Cys Ser
65 70 75
Cys Gln Cys Pro Ala Ala Met Ala Phe Cys Phe Leu Glu Thr Leu
80 85 90
Trp Trp Glu Phe Thr Ala Ser Tyr Asp Thr Thr Cys Ile Gly Leu
95 100 105
Ala Ser Arg Pro Tyr Ala Phe Leu Glu Phe Asp Ser Ile Ile Gln
110 115 120
Lys Val Lys Trp His Phe Asn Tyr Val Ser Ser Ser Gln Met Glu
125 130 135
Cys Ser Leu Glu Lys Ile Gln Glu Glu Leu Lys Leu Gln Pro Pro
140 145 150
Ala Val Leu Thr Leu Glu Asp Thr Asp Val Ala Asn Gly Val Met
155 160 165
Asn Gly His Thr Pro Met His Leu Glu Pro Ala Pro Asn Phe Arg
170 175 180
Met Glu Pro Val Thr Ala Leu Gly Ile Leu Ser Leu Ile Leu Asn
185 190 195
Ile Met Cys Ala Ala Leu Asn Leu Ile Arg Gly Val His Leu Ala
200 205 210
Glu His Ser Leu Gln Asp Pro Arg Ser Trp Phe Cys Trp Leu Asp
215 220 225
Gln Thr Ser

<210> 136
<211> 239
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 39, 61, 143, 209
<223> unknown base

<400> 136
tgcttcctgg agaccctgtg gtgggaattc acagcttcnt atgacactac 50
ctgcattggc nttagctcca ggccatacgc ttttctttag tttgacagca 100
tcattcagaa agtgaagtgg cattttaact atgtaagttc ctntcagatg 150
gagtgcagct tgaaaaaat tcaggaggag ctcagaattgc agccctccagc 200
ggtttcant atggaggaca cagatgtggc aaatgggt 239

<210> 137
<211> 2300
<212> DNA

<213> Homo sapiens

<400> 137
ctcagccgc cttccctcgta gcgagccctag tggccgggtgt ttgcattgaa 50
acgtgagcgc gacccgcacct taaagagtgg ggagcaaaagg gaggacagag 100
ccctttaaaaa cgaggccgggt ggtgcctgcc cctttaagggg cggggcggtcc 150
ggacgactgt atctgagccc cagactgccc cgagttctg tcgcaggctg 200
cgaggaaagg ccccttaggct gggtctgggt gcttggccgc ggcggcttcc 250
tcccccgctcg tccctcccgcc gcccagggc acctcggtt cagtcatgtc 300
gagcagagta tggaaagcacc tgactacgaa gtgcataccg tgcgagaaca 350
gtcttccac gagaggatcc gcgagtgat tatataaca ctctgtttg 400
caacactgta catcctctgc cacatcttc tgaccgcctt caagaagct 450
gctgagttca ccacagtggta tgatgaagat gccacccgtca acaagattgc 500
gctcgagctg tgacaccccta ccctggcaat tgccctgggt gtcgtctgc 550
tcctggccctt ctccatcatc agcaatgagg tgctgctctc cctgcctcg 600
aactactaca tccagtggtc caacggctcc ctcatccatg gcctctggaa 650
ccctgtttt ctctcccca acctgtccctt catcttcctc atgccttttg 700
catatttctt cactgagtct gagggtttt ctggctccag aaagggtgtc 750
ctggcccggt tctatgagac agtgggtatg ttgtatgtcc tcaactctgt 800
ggtgcttagt atggtgtggg tggcatcagc catttggac aagaacaagg 850
ccaacagaga gtcactctat gacttttggg agtactatct cccctacctc 900
tactcatgca tctcccttctt tggggttctg ctgctctgg tttgtactcc 950
actgggttcc tcccgcatgt tctccgtcac tggaaagctg ctatgtcaagg 1000
cccggtctgtc ggaagacctg gaggagcagc tgactgtctc agccttttag 1050
gaggcagccc tgaccccgac gatctgtat cctacttccct gctggctgcc 1100
tttagacatg gagctgtac acagacagg tctggctctg cagacacaga 1150
gggtcctgtc ggagaagagg cggaaaggctt cagcctggca acggaaacctg 1200
ggctacccccc tggctatgtc gtgttgcgtc gtgtgtacgg gcctgtctgt 1250
gctcatttgtc gccatccaca tccctggagct gctcatcgat gaggctgcca 1300
tgcccccggg catgcagggtt acctcccttag gcagggtctc cttctccaag 1350
ctgggctccctt tgggtggcgtt cattcaggtt gtactcatct tttacctaatt 1400
gggtgcctca gtttgggtt tctatagctc tccacttccctt cggagccctgc 1450
ggcccagatg gcacgcacact gccatgcacgc agataattgg gaactgtgtc 1500

tgtctcctgg tcctaagctc agcacttcct gtcttctc gaaccctggg 1550
gctcactcg tttgacactc tgggtgactt tggacgcttc aactggctgg 1600
gcaatttcta catttgttgc ctctacaacg cagccttgc aggccctcacc 1650
acactctgtc tggtaagac cttcaactgca gctgtgcggg cagagctgat 1700
ccggccctt gggctggaca gactgcccgc gcccgtctcc ggtttcccc 1750
aggcatctag gaagacccag caccagtac ctccagctgg gggtgaaaag 1800
aaaaaaactg gacactgcca tctgctgcctt aggccctggag ggaagcccaa 1850
ggctacttgg acctcaggac ctgaaatctg agagggtggg tggcagaggg 1900
gagcagagcc atctcgacta ttgcataatc tgagccagag tttgggacca 1950
ggacctcctg cttttccata cttaactgtg gcctcagcat ggggtaggc 2000
tgggtactg ggtctagcccc ctgatcccaa atctgtttac acatcaatct 2050
gcctcaactgc tggctctggc catccccata gccatgttta catgattga 2100
tgtgcaatag ggtggggtag gggcaggaa aggactggc cagggcaggc 2150
tcggagata gattgtctcc ctgcctctg gcccagcaga gcctaagcac 2200
tgtgctatcc tggaggggct ttggaccacc taaaagacca aggggatagg 2250
gaggaggagg cttcagccat cagcaataaa gttgatccca gggaaaaaaaa 2300

<210> 138
<211> 489
<212> PRT
<213> Homo sapiens

<400> 138
Met Glu Ala Pro Asp Tyr Glu Val Leu Ser Val Arg Glu Gln Leu
1 5 10 15
Phe His Glu Arg Ile Arg Glu Cys Ile Ile Ser Thr Leu Leu Phe
20 25 30
Ala Thr Leu Tyr Ile Leu Cys His Ile Phe Leu Thr Arg Phe Lys
35 40 45
Lys Pro Ala Glu Phe Thr Thr Val Asp Asp Glu Asp Ala Thr Val
50 55 60
Asn Lys Ile Ala Leu Glu Leu Cys Thr Phe Thr Leu Ala Ile Ala
65 70 75
Leu Gly Ala Val Leu Leu Leu Pro Phe Ser Ile Ile Ser Asn Glu
80 85 90
Val Leu Leu Ser Leu Pro Arg Asn Tyr Tyr Ile Gln Trp Leu Asn
95 100 105
Gly Ser Leu Ile His Gly Leu Trp Asn Leu Val Phe Leu Phe Pro
110 115 120
Asn Leu Ser Leu Ile Phe Leu Met Pro Phe Ala Tyr Phe Phe Thr

TOP SECRET//NOFORN

125	130	135
Glu Ser Glu Gly Phe Ala Gly Ser Arg Lys Gly Val Leu Gly Arg		
140	145	150
Val Tyr Glu Thr Val Val Met Leu Met Leu Leu Thr Leu Leu Val		
155	160	165
Leu Gly Met Val Trp Val Ala Ser Ala Ile Val Asp Lys Asn Lys		
170	175	180
Ala Asn Arg Glu Ser Leu Tyr Asp Phe Trp Glu Tyr Tyr Leu Pro		
185	190	195
Tyr Leu Tyr Ser Cys Ile Ser Phe Leu Gly Val Leu Leu Leu Leu		
200	205	210
Val Cys Thr Pro Leu Gly Leu Ala Arg Met Phe Ser Val Thr Gly		
215	220	225
Lys Leu Leu Val Lys Pro Arg Leu Leu Glu Asp Leu Glu Glu Gln		
230	235	240
Leu Tyr Cys Ser Ala Phe Glu Glu Ala Ala Leu Thr Arg Arg Ile		
245	250	255
Cys Asn Pro Thr Ser Cys Trp Leu Pro Leu Asp Met Glu Leu Leu		
260	265	270
His Arg Gln Val Leu Ala Leu Gln Thr Gln Arg Val Leu Leu Glu		
275	280	285
Lys Arg Arg Lys Ala Ser Ala Trp Gln Arg Asn Leu Gly Tyr Pro		
290	295	300
Leu Ala Met Leu Cys Leu Leu Val Leu Thr Gly Leu Ser Val Leu		
305	310	315
Ile Val Ala Ile His Ile Leu Glu Leu Leu Ile Asp Glu Ala Ala		
320	325	330
Met Pro Arg Gly Met Gln Gly Thr Ser Leu Gly Gln Val Ser Phe		
335	340	345
Ser Lys Leu Gly Ser Phe Gly Ala Val Ile Gln Val Val Leu Ile		
350	355	360
Phe Tyr Leu Met Val Ser Ser Val Val Gly Phe Tyr Ser Ser Pro		
365	370	375
Leu Phe Arg Ser Leu Arg Pro Arg Trp His Asp Thr Ala Met Thr		
380	385	390
Gln Ile Ile Gly Asn Cys Val Cys Leu Leu Val Leu Ser Ser Ala		
395	400	405
Leu Pro Val Phe Ser Arg Thr Leu Gly Leu Thr Arg Phe Asp Leu		
410	415	420
Leu Gly Asp Phe Gly Arg Phe Asn Trp Leu Gly Asn Phe Tyr Ile		
425	430	435
Val Phe Leu Tyr Asn Ala Ala Phe Ala Gly Leu Thr Thr Leu Cys		

TIGRIS

440	445	450
Leu Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu Ile Arg 455	460	465
Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe Pro 470	475	480
Gln Ala Ser Arg Lys Thr Gln His Gln 485		

<210> 139
<211> 294
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 53, 57
<223> unknown base

<400> 139
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ggnttcntcc ccgctcgccc tccccgggccc cagaggcacc tcggcttcag 100
tcatgtcttag cagatgtatgg aagcacctga ctacgaagtgc ctatccgtgc 150
gagaacacgtt attcacacgag aggtatcccgcg agtgttatatt atcaacactt 200
ctgtttgcaaa cactgtacat cctctgccc acatcttcgtt cccgcttcaa 250
gaagcctgtt gagttcacca cagtggatga tgaagatgcc accg 294

<210> 140
<211> 526
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 197, 349
<223> unknown base

<400> 140
gaccgacccat aaagagtggg agcaaaggga ggacagagcc ttttaaaaacg 50
aggccgttggc gcctggccctt taagggggggg gcgtccggac gactgtatct 100
gagcccccaga ctgcccccgag tttctgtcgcc aggctgcgag gaaaggcccc 150
taggctgggt ctggtgcttg cggccggcgg ctctccccc gttgtcnccc 200
ccggggcccg aggcacccctcg gttcagtc tgctgagcag agtatggaaag 250
cacctgacta cgaagtgcata tccgtgcgag aacagctatt ccacgagagg 300
atccgcgagt gtattatatac aacacccatctt tttgcaacac ttttgcacatn 350
ctggccacatc ttccctgaccc gtttcaagaaa gcctgcttag tttcaccacag 400
tggatgtatga agatgccacc gcacaaaga ttgcgtcgat gctgtgcacc 450

tttaccctgg caattgccct ggggtgtc ctgctctgc ctttccat 500
catcagaat gaggtgtc actccc 526

<210> 141
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 141
gactgtatct gagccccaga ctgc 24

<210> 142
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 142
tcagcaatga ggtgtgtc 20

<210> 143
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 143
tgaggaagat gagggacagg ttgg 24

<210> 144
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 144
tatggaaagca cctgactacg aagtgtatc cggtcgagaa cagctattcc 50

<210> 145
<211> 685
<212> DNA
<213> Homo sapiens

<400> 145
gatgtgctcc ttggagctgg tgtgcagtgt cctgactgta agatcaagtc 50
caaacctgtt ttggaaattga ggaaacttct cttttgatct cagcccttgg 100
tggtccagggt cttcatgtcg ctgtgggtga tattactggt cctggctct 150
gtcagtgac agtttgcacg gacacccagg cccattattt tcctccagcc 200
tccatggacc acagtcttcc aaggagagag agtgaccctc acttgcaagg 250

gatttcgtt ctactcacca cagaaaacaa aatggatcca tgggtaccc 300
 gggaaagaaa tactaagaga aaccccagac aatatccctg aggttcagg 350
 atctggagag tacagatgcc aggcccagg ctccccctc agtagccctg 400
 tgcaaccttga ttttcttca gagatggat ttccatgc tgcccatgc 450
 aatgttgaac tcctgggctc aagtgtatcg ctcacccatgg cctctcaaag 500
 cgctgggatt acagcttcgc tgatcctgc agtcccatct tctgtgttg 550
 aaggagactc tgtggttctg aggtgcggg caaaggcggg agtaacactg 600
 ataataacta tttacaagaa tgataatgtc ctggcatcc ttaataaaaag 650
 aactgacttc caaaaaaaaaaaaaaa 685

<210> 146

<211> 124

<212> PRT

<213> Homo sapiens

<400> 146

Met	Leu	Leu	Trp	Val	Ile	Leu	Leu	Val	Leu	Ala	Pro	Val	Ser	Gly
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Gln	Phe	Ala	Arg	Thr	Pro	Arg	Pro	Ile	Ile	Phe	Leu	Gln	Pro	Pro
	20								25					30

Trp	Thr	Thr	Val	Phe	Gln	Gly	Glu	Arg	Val	Thr	Leu	Thr	Cys	Lys
			35						40					45

Gly	Phe	Arg	Phe	Tyr	Ser	Pro	Gln	Lys	Thr	Lys	Trp	Tyr	His	Arg
			50						55					60

Tyr	Leu	Gly	Lys	Glu	Ile	Leu	Arg	Glu	Thr	Pro	Asp	Asn	Ile	Leu
		65						70					75	

Glu	Val	Gln	Glu	Ser	Gly	Glu	Tyr	Arg	Cys	Gln	Ala	Gln	Gly	Ser
		80							85					90

Pro	Leu	Ser	Ser	Pro	Val	His	Leu	Asp	Phe	Ser	Ser	Glu	Met	Gly
				95					100					105

Phe	Pro	His	Ala	Ala	Gln	Ala	Asn	Val	Glu	Leu	Leu	Gly	Ser	Ser
				110					115					120

Asp Leu Leu Thr

<210> 147

<211> 1621

<212> DNA

<213> Homo sapiens

<400> 147

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cccccccggt	gtgaggccgg	ctcacaggcc	cggttggct	ggcgagccga	100
------------	------------	------------	-----------	------------	-----

cgccggccgc	gaggaggctg	tgaggagtgt	gtggAACAGG	acccgggaca	150
------------	------------	------------	------------	------------	-----

卷之三

gaggaaaccat ggctccggcag aacctcgacca cttttgcctt gttgtcgcta 200
tacctcatcg gggcggtgat tgccggacga gattttata agatcttggg 250
ggtgccctcgta agtgccctcta taaaaggatata taaaaggcc tatagggaaac 300
tagccctcgca gtttcattccc gaccggaaacc ctgtatgtatcc acaagcccc 350
gagaaattcc aggtatctggg tgctgtttat gaggttctgtt cagatagtga 400
gaaacggaaa cgtacgata cttatggtga agaaggatta aaagatggtc 450
atcagagtc ccatggagac atttttcac acttcttggg ggattttgtt 500
ttcatgtttg gaggaaacccc tcgtcagcaa gacagaaata ttccaagagg 550
aagtatgttattt attgttagatc tagaagtacat ttggaaagaa gtatatgcg 600
gaaattttgtt ggaagtagtt agaaacaaac ctgtggcaag gcaggctct 650
ggcaaacggaa agtgcatttgc tcggcaagag atgcggacca cccagctggg 700
ccctggcgc ttccaaatga cccaggaggt ggtctgcac gaatggccata 750
atgtcaactt agtgaatgaa gaacgaacgc ttggaaagttt aatagagct 800
gggggtgagag acggcatgga gtacccctttt attggagaag gtgagcccta 850
cgtggatggg gaggctggag attacgggtt ccgaatcaa ttgttcaagc 900
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ttggtcacaaag gtacatattt cccggataa gatcaccagg ccaggagcg 1050
agctatggaa gaaagggaa gggtccccca actttgacaa caacaatatac 1100
aagggtcttt tgataatcac tttgtatgtt gatTTTCAA aagaacagtt 1150
aacagaggaa gcgagagaag gtatcaaaca gctactgaaa caagggtcg 1200
tgcagaaggtt atacaatggat ctgcaaggat attgagatgtt aataaaattt 1250
gactttgtttt aaaataagttt aataagcgat atttattatc tgcagggttt 1300
tttttgtgtt ttatTTTCAA tatgcaagttt aggcttaattt 1350
tttttatcta atgatcatca tggaaatgtt aagagggtt aagaattttt 1400
ccatttgcat tcggaaaaga atgaccagca aaggtttac taatactct 1450
ccctttgggg atttaatgtc ttgtgtcgcc gctcgatgtt caagaattaa 1500
agctgcagaaga ggactccagg agccaaagaa acacaatata gagggttgg 1550
ttgtttagca atttcattca aatgccaac tggagaagtc ttgtttttaaa 1600
tacattttgtt ttgtttttttt a 1621

<210> 148
<211> 358
<212> PBT

<213> Homo sapiens

<400> 148

Met Ala Pro Gln Asn Leu Ser Thr Phe Cys Leu Leu Leu Tyr	10	15
1	5	
Leu Ile Gly Ala Val Ile Ala Gly Arg Asp Phe Tyr Lys Ile Leu	25	30
20		
Gly Val Pro Arg Ser Ala Ser Ile Lys Asp Ile Lys Lys Ala Tyr	40	45
35		
Arg Lys Leu Ala Leu Gln Leu His Pro Asp Arg Asn Pro Asp Asp	55	60
50		
Pro Gln Ala Gln Glu Lys Phe Gln Asp Leu Gly Ala Ala Tyr Glu	70	75
65		
Val Leu Ser Asp Ser Glu Lys Arg Lys Gln Tyr Asp Thr Tyr Gly	85	90
80		
Glu Glu Gly Leu Lys Asp Gly His Gln Ser Ser His Gly Asp Ile	100	105
95		
Phe Ser His Phe Phe Gly Asp Phe Gly Phe Met Phe Gly Gly Thr	115	120
110		
Pro Arg Gln Gln Asp Arg Asn Ile Pro Arg Gly Ser Asp Ile Ile	130	135
125		
Val Asp Leu Glu Val Thr Leu Glu Glu Val Tyr Ala Gly Asn Phe	145	150
140		
Val Glu Val Val Arg Asn Lys Pro Val Ala Arg Gln Ala Pro Gly	160	165
155		
Lys Arg Lys Cys Asn Cys Arg Gln Glu Met Arg Thr Thr Gln Leu	175	180
170		
Gly Pro Gly Arg Phe Gln Met Thr Gln Glu Val Val Cys Asp Glu	190	195
185		
Cys Pro Asn Val Lys Leu Val Asn Glu Glu Arg Thr Leu Glu Val	205	210
200		
Glu Ile Glu Pro Gly Val Arg Asp Gly Met Glu Tyr Pro Phe Ile	220	225
215		
Gly Glu Gly Glu Pro His Val Asp Gly Glu Pro Gly Asp Leu Arg	235	240
230		
Phe Arg Ile Lys Val Val Lys His Pro Ile Phe Glu Arg Arg Gly	250	255
245		
Asp Asp Leu Tyr Thr Asn Val Thr Ile Ser Leu Val Glu Ser Leu	265	270
260		
Val Gly Phe Glu Met Asp Ile Thr His Leu Asp Gly His Lys Val	280	285
275		
His Ile Ser Arg Asp Lys Ile Thr Arg Pro Gly Ala Lys Leu Trp	295	300

Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp Asn Asn Ile Lys
305 310 315
Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe Pro Lys Glu Gln
320 325 330 335
Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu Leu Lys Gln
335 340 345
Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr
350 355

<210> 149
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 34, 52, 134, 142, 155, 158, 196, 217, 228, 272, 347, 410, 445,
482
<223> unknown base

<400> 149
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gntgcgaccg aagccggcggg cgaggaggat tttgaggatt tttggaacag 100
gaccggaca gaggAACAT ggcccgccag aacntgagca ctttttgct 150
gttgtntata tacttcatcg gggccgtat tgccggacga gattttntata 200
agatTTGGG gtgcctngaa gtgcctnta taaaggatata taaaaggcc 250
tatAGGAACAC tagccctgca gntttatccc gaccggaaacc ctgatgatcc 300
acaAGCCCAAG gagaAAATTCC aggatTTGGG tgctgtttat gaggtttgt 350
cagatAGTGA gaaACGGAAA cagtacgata attatGGTGA agaaggattta 400
aaAGATGGTAT atcAGAGCTC ccatggagac attttttcac acttttttg 450
ggatTTGGT ttcatgtttg gaggAACCCC tngtcagcaa gacagaaata 500
ttccaagag 509

<210> 150
<211> 1532
<212> DNA
<213> Homo sapiens

<400> 150
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ctcttccca atttgccact tccagcagct ttagcccatg aggaggatgt 150
gaccgggact gagtcaggag ccctctggaa gcatggagac tgggtgtatt 200
gttgcctatag gtgtcgatggc caccatcttt ctggcttcgtt ttcgcagccct 250
ggtgctgggtt tgcaggcagc gctactgccc gccgcgagac ctgctgcagc 300

gctatgattc taagccatt gtggaccta ttgggccat ggagacccag 350
tctgagccct ctgagttaga actggacgt gtcgttatca ccaacccca 400
cattgaggcc attctggaga atgaagactg gatcgaaatg gctcgggtc 450
tcatgtccca ctgcattgc acatcgaaa tttgtcacac tctgacagag 500
aagcttggccatg ccatgacaat gggctctggg gccaagatga agacttcaggc 550
cagtgtcaggc gacatcgatgg tggggccaa gggatcgaccccagggtgg 600
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<210> 151

<211> 226

<212> PRT

<213> Homo sapiens

<400> 151

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20 25 30

Tyr Cys Arg Pro Arg Asp Leu Leu Gln Arg Tyr Asp Ser Lys Pro

DRAFT

35

40

45

Ile	Val	Asp	Leu	Ile	Gly	Ala	Met	Glu	Thr	Gln	Ser	Glu	Pro	Ser
50								55					60	
Glu	Leu	Glu	Leu	Asp	Asp	Val	Val	Ile	Thr	Asn	Pro	His	Ile	Glu
65								70					75	
Ala	Ile	Leu	Glu	Asn	Glu	Asp	Trp	Ile	Glu	Asp	Ala	Ser	Gly	Leu
80								85					90	
Met	Ser	His	Cys	Ile	Ala	Ile	Leu	Lys	Ile	Cys	His	Thr	Leu	Thr
95								100					105	
Glu	Lys	Leu	Val	Ala	Met	Thr	Met	Gly	Ser	Gly	Ala	Lys	Met	Lys
110								115					120	
Thr	Ser	Ala	Ser	Val	Ser	Asp	Ile	Ile	Val	Val	Ala	Lys	Arg	Ile
125								130					135	
Ser	Pro	Arg	Val	Asp	Asp	Val	Val	Lys	Ser	Met	Tyr	Pro	Pro	Leu
140								145					150	
Asp	Pro	Lys	Leu	Leu	Asp	Ala	Arg	Thr	Thr	Ala	Leu	Leu	Leu	Ser
155								160					165	
Val	Ser	His	Leu	Val	Leu	Val	Thr	Arg	Asn	Ala	Cys	His	Leu	Thr
170								175					180	
Gly	Gly	Leu	Asp	Trp	Ile	Asp	Gln	Ser	Leu	Ser	Ala	Ala	Glu	Glu
185								190					195	
His	Leu	Glu	Val	Leu	Arg	Glu	Ala	Ala	Leu	Ala	Ser	Glu	Pro	Asp
200								205					210	
Lys	Gly	Leu	Pro	Gly	Pro	Glu	Gly	Phe	Leu	Gln	Glu	Gln	Ser	Ala
215								220					225	

Ile

<210> 152
<211> 1027
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1017, 1020
<223> unknown base

<400> 152
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aaaattggaa tggttggaa aggattttggaa gtgtttttcc ttgtttttgg 150
aatgatttctc ttgttttgcaca aagcactact ggctattggaa aatgttttat 200
ttgttagccgg ctggcgtttt gtaatgggtt tagaaagaac attcagattc 250
ttcttccaaa aacataaaat gaaagctaca ggttttttcc tgggtgggtgt 300

atttgttagtc cttattgggtt ggccttgat aggcataatc ttcgaaat 350
atggatTTT tctcttggtc aggggcttct ttccctgtcg tggtggctt 400
attagaagag tgccagtcc tggatccctc ctaaattac ctggaattag 450
atcatTTTA gataaaagtgtt gagaaagcaa caaatatggta taacaacaag 500
tgaatttggaa gactcattta aaatattgtt ttatttataa agtcatttga 550
agaatattca gcacaaaatt aaattacatg aaatagctt taatgttctt 600
tacaggagggt taaaacgtat agcctacaaa gtaccagcag caaattagca 650
aagaaggcgt gaaaacaggc ttctactcaa gtgaactaag aagaagttag 700
caagcaact gagagagggtt aaatccatgt taatgtatgt taagaactc 750
ttgaaggcta ttgtgttgtt tttccacaa tgcgtggaaac tcagccatcc 800
tttagagaact gtgggtccty tttctttctt ttttattttt aaggctcagg 850
agcatccata ggcatttgc ttttagaaagt gtccactgca atggcaaaaa 900
tatTTCCAGT tgcactgtat ctctggaaagt gatgcataa ttcgatTTGA 950
ttgtgtcatt ttaaagtatt aaacccaagg aaaccccaat ttgtatgtat 1000
ggattacttt ttttgnncn cagggcc 1027

<210> 153
<211> 138
<212> PRT
<213> Homo sapiens

<220>
<221> N-myristoylation Sites
<222> 11-16, 51-56 and 116-121
<223> N-myristoylation Sites.

<220>
<221> Transmembrane domains
<222> 12-30, 33-52, 69-89 and 93-109
<223> Transmembrane domains

<220>
<221> Aminoacyl-transfer RNA Synthetases.
<222> 49-59
<223> Aminoacyl-transfer RNA synthetases class-II protein.

<400> 153
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20 25 30
Asp Lys Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly
35 40 45
Leu Ala Phe Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe
50 55 60

Gln Lys His Lys Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val
65 70 75
Phe Val Val Leu Ile Gly Trp Pro Leu Ile Gly Met Ile Phe Glu
80 85 90
Ile Tyr Gly Phe Phe Leu Leu Phe Arg Gly Phe Phe Pro Val Val
95 100 105
Val Gly Phe Ile Arg Arg Val Pro Val Leu Gly Ser Leu Leu Asn
110 115 120
Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val Gly Glu Ser Asn
125 130 135

Asn Met Val

<210> 154
<211> 405
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 66
<223> unknown base

<400> 154
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ttaaccggat ttggagtgtt ttccctgttc tttggatga ttctcttttt 200
tgacaaagca ctactggcta ttggaaatgt ttatattgtt gccggcttgg 250
cttttgtataa tgggttagaa agaacattca gattttctt ccaaaaacat 300
aaaatgaaag ctacagggtt tttctgggt ggttatgg tagtccttat 350
tggttggcct ttatagggca tgatcttgcgaa aatttatggaa tttttctct 400
tgttc 405

<210> 155
<211> 1781
<212> DNA
<213> Homo sapiens

<400> 155
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tttcttcctt ctggaaatct ttgactgtgg gtagttattt atttctgaat 150
aagagcgtcc acgcatcatg gacctcgccg gactgctgaa gtctcgttgcata 200
ctgtgccacc tggcttcgtt ctacgtctt attgcctcag ggctaatcat 250

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caacaccatt cagcttca ctcttcctct ctggccatt aacaaggcago 300
tctccggaa gatcaactgc agactgtctt attgcatctc aagccagctg 350
gtgtatgtgc tggagtgggt gtggggcacg gaatgcacca tttcacgg 400
cccccgcc tacctaagt atgggaagga aaatgcattt gtgtttctca 450
accacaagtt tgaatttgac ttcttgtgtg gtggggccct gtccgaacgc 500
tttgggctgt tagggggctc caaggctctt gccaagaag agctggccta 550
tgtcccaatt atccgttgc tggttactt caccggatgt gtcttcgtt 600
cgcgcaagtggagcaggat cgcaagacgg ttgccaccag ttgcagcac 650
ctccggact acccccggaaa gtatttttc ctgttactt gtggggcac 700
acgggttacgg gagaagaagc atgagatcag catcgagggtt gcccggcc 750
aggggcttgc tcgcctcaag catcacctgt tgccacgaac caaggcttc 800
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<210> 156

<211> 378
<212> PRT
<213> Homo sapiens

<400> 156
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35 40 45
Phe Arg Lys Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser Gln
50 55 60
Leu Val Met Leu Leu Glu Trp Trp Ser Gly Thr Glu Cys Thr Ile
65 70 75
Phe Thr Asp Pro Arg Ala Tyr Leu Lys Tyr Gly Lys Glu Asn Ala
80 85 90
Ile Val Val Leu Asn His Lys Phe Glu Ile Asp Phe Leu Cys Gly
95 100 105
Trp Ser Leu Ser Glu Arg Phe Gly Leu Leu Gly Gly Ser Lys Val
110 115 120
Leu Ala Lys Lys Glu Leu Ala Tyr Val Pro Ile Ile Gly Trp Met
125 130 135
Trp Tyr Phe Thr Glu Met Val Phe Cys Ser Arg Lys Trp Glu Gln
140 145 150
Asp Arg Lys Thr Val Ala Thr Ser Leu Gln His Leu Arg Asp Tyr
155 160 165
Pro Glu Lys Tyr Phe Phe Leu Ile His Cys Glu Gly Thr Arg Phe
170 175 180
Thr Glu Lys Lys His Glu Ile Ser Met Gln Val Ala Arg Ala Lys
185 190 195
Gly Leu Pro Arg Leu Lys His His Leu Leu Pro Arg Thr Lys Gly
200 205 210
Phe Ala Ile Thr Val Arg Ser Leu Arg Asn Val Val Ser Ala Val
215 220 225
Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu
230 235 240
Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu Tyr Val
245 250 255
Arg Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu Cys
260 265 270
Ser Ala Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Phe Gln
275 280 285
Glu Glu Tyr Tyr Arg Thr Gly Thr Phe Pro Glu Thr Pro Met Val

290	295	300
Pro Pro Arg Arg Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala		
305	310	315
Ser Leu Val Leu Tyr Pro Phe Phe Gln Phe Leu Val Ser Met Ile		
320	325	330
Arg Ser Gly Ser Ser Leu Thr Leu Ala Ser Phe Ile Leu Val Phe		
335	340	345
Phe Val Ala Ser Val Gly Val Arg Trp Met Ile Gly Val Thr Glu		
350	355	360
Ile Asp Lys Gly Ser Ala Tyr Gly Asn Ser Asp Ser Lys Gln Lys		
365	370	375

Leu Asn Asp

<210> 157

<211> 1849

<212> DNA

<213> Homo sapiens

<400> 157

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 tactgattcc caaatggatg atgttgaagt tgtttataaca attgacattc 200
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 tacataagat aaatgaaatg tatgcttcat tacaagggatg attaaagagt 700
 atatgcaaaa aagtggaaaga cagtgaacaa gcagtagata aacttagataa 750
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 ttcatgtgtttt atgtctttaa aaaatagaca tgtttctaaa agtagctgta 950

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actacaacca ccatctcgat tggtagagaca atctgacccat aatggtagaa 1000
cacactgaca ttccctgaagc tagtccagct agtacaccac aaatcattaa 1050
gcataaaagcc ttagacttag atgacagatg gcaattaacg agatctcggt 1100
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aaatttgcacaa aacatcatct aaaattttaa aaaaaaaaaa aaaaaaaaaa 1849

<210> 158
<211> 409
<212> PRT
<213> *Homo sapiens*

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 110 115 120
 Leu Gln Glu His Phe Ser Asn Gln Asp Leu Val Phe Leu Leu Leu
 125 130 135
 Thr Pro Ser Ile Ile Thr Glu Ser Cys Ser Thr His Arg Leu Glu
 140 145 150
 His Ser Leu Tyr Lys Pro Gln Lys Gly Leu Phe His Arg Val Pro
 155 160 165
 Leu Val Val Ala Asn Leu Gly Met Ser Glu Gln Leu Gly Tyr Lys
 170 175 180
 Thr Val Ser Gly Ser Cys Met Ser Thr Gly Phe Ser Arg Ala Val
 185 190 195
 Gln Thr His Ser Ser Lys Phe Phe Glu Glu Asp Gly Ser Leu Lys
 200 205 210
 Glu Val His Lys Ile Asn Glu Met Tyr Ala Ser Leu Gln Glu Glu
 215 220 225
 Leu Lys Ser Ile Cys Lys Lys Val Glu Asp Ser Glu Gln Ala Val
 230 235 240
 Asp Lys Leu Val Lys Asp Val Asn Arg Leu Lys Arg Glu Ile Glu
 245 250 255
 Lys Arg Arg Gly Ala Gln Ile Gln Ala Ala Arg Glu Lys Asn Ile
 260 265 270
 Gln Lys Asp Pro Gln Glu Asn Ile Phe Leu Cys Gln Ala Leu Arg
 275 280 285
 Thr Phe Phe Pro Asn Ser Glu Phe Leu His Ser Cys Val Met Ser
 290 295 300
 Leu Lys Asn Arg His Val Ser Lys Ser Ser Cys Asn Tyr Asn His
 305 310 315
 His Leu Asp Val Val Asp Asn Leu Thr Leu Met Val Glu His Thr
 320 325 330
 Asp Ile Pro Glu Ala Ser Pro Ala Ser Thr Pro Gln Ile Ile Lys
 335 340 345
 His Lys Ala Leu Asp Leu Asp Asp Arg Trp Gln Phe Lys Arg Ser
 350 355 360
 Arg Leu Leu Asp Thr Gln Asp Lys Arg Ser Lys Ala Asn Thr Gly
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 Ser Ser Asn Gln Asp Lys Ala Ser Lys Met Ser Ser Pro Glu Thr
 380 385 390
 Asp Glu Glu Ile Glu Lys Met Lys Gly Phe Gly Glu Tyr Ser Arg
 395 400 405
 Ser Pro Thr Phe

<210> 159
<211> 2651
<212> DNA
<213> *Homo sapiens*

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ttcccccggt ccccgccctcg ccggccatgc agcttgcggg gttcgctgcc 200
cccgaaacc ccggaggctac cagcccgccg ctctgttcc ctggcccg 250
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agtgtggtca gcaaacatgtg caatcatgg aagctgtct ttgtttcacg 800
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cttcaaca ttqaatcggtt catggatccc atcgatgtga 1450

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cagaagggtt tccaggatg tggacccccc aagccccctcc cagctggacg 1550
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actgtgcattt gagttggttc ctgtccccccaaaccatgtt aaacgtggct 2400
aacatgttagt gtacagaact atagttatgtt gtgcattttgtt gattttatca 2450
ctctattattt tttttttctc atttcgttttggg tgggtttttt 2500
tttccaactg tgatctcgcc ttgtttctta caagcaaaacc agggccctt 2550
cttggcacgt aacatgtacg tattttctgaa atattaaata gctgtacaga 2600
agcagggtttt atttatcatgtt ttatcttattt aaaagaaaaa gccccaaaaag 2650
c 2651

<210> 160
<211> 556
<212> PRT
<213> Homo sapiens

<400> 160
Met Ala Arg Phe Gly Leu Pro Ala Leu Leu Cys Thr Leu Ala Val
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Leu Ser Ala Ala Leu Leu Ala Ala Glu Leu Lys Ser Lys Ser Cys
20 25 30
Ser Glu Val Arg Arg Leu Tyr Val Ser Lys Gly Phe Asn Lys Asn

TOPIC: PROTEIN

35	40	45
Asp Ala Pro Leu His Glu Ile Asn Gly Asp His Leu Lys Ile Cys		
50	55	60
Pro Gln Gly Ser Thr Cys Cys Ser Gln Glu Met Glu Glu Lys Tyr		
65	70	75
Ser Leu Gln Ser Lys Asp Asp Phe Lys Ser Val Val Ser Glu Gln		
80	85	90
Cys Asn His Leu Gln Ala Val Phe Ala Ser Arg Tyr Lys Lys Phe		
95	100	105
Asp Glu Phe Phe Lys Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu		
110	115	120
Asn Asp Met Phe Val Lys Thr Tyr Gly His Leu Tyr Met Gln Asn		
125	130	135
Ser Glu Leu Phe Lys Asp Leu Phe Val Glu Leu Lys Arg Tyr Tyr		
140	145	150
Val Val Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp		
155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Arg Leu Val Asn Ser Gln Tyr		
170	175	180
His Phe Thr Asp Glu Tyr Leu Glu Cys Val Ser Lys Tyr Thr Glu		
185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Leu Gln		
200	205	210
Val Thr Arg Ala Phe Val Ala Ala Arg Thr Phe Ala Gln Gly Leu		
215	220	225
Ala Val Ala Gly Asp Val Val Ser Lys Val Ser Val Val Asn Pro		
230	235	240
Thr Ala Gln Cys Thr His Ala Leu Leu Lys Met Ile Tyr Cys Ser		
245	250	255
His Cys Arg Gly Leu Val Thr Val Lys Pro Cys Tyr Asn Tyr Cys		
260	265	270
Ser Asn Ile Met Arg Gly Cys Leu Ala Asn Gln Gly Asp Leu Asp		
275	280	285
Phe Glu Trp Asn Asn Phe Ile Asp Ala Met Leu Met Val Ala Glu		
290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile		
305	310	315
Asp Val Lys Ile Ser Asp Ala Ile Met Asn Met Gln Asp Asn Ser		
320	325	330
Val Gln Val Ser Gln Lys Val Phe Gln Gly Cys Gly Pro Pro Lys		
335	340	345
Pro Leu Pro Ala Gly Arg Ile Ser Arg Ser Ile Ser Glu Ser Ala		

DRAFT STRAIN 600

350	355	360
Phe Ser Ala Arg Phe Arg Pro His His Pro Glu Glu Arg Pro Thr		
365	370	375
Thr Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Val Lys		
380	385	390
Glu Lys Leu Lys Gln Ala Lys Lys Phe Trp Ser Ser Leu Pro Ser		
395	400	405
Asn Val Cys Asn Asp Glu Arg Met Ala Ala Gly Asn Gly Asn Glu		
410	415	420
Asp Asp Cys Trp Asn Gly Lys Gly Lys Ser Arg Tyr Leu Phe Ala		
425	430	435
Val Thr Gly Asn Gly Leu Ala Asn Gln Gly Asn Asn Pro Glu Val		
440	445	450
Gln Val Asp Thr Ser Lys Pro Asp Ile Leu Ile Leu Arg Gln Ile		
455	460	465
Met Ala Leu Arg Val Met Thr Ser Lys Met Lys Asn Ala Tyr Asn		
470	475	480
Gly Asn Asp Val Asp Phe Phe Asp Ile Ser Asp Glu Ser Ser Gly		
485	490	495
Glu Gly Ser Gly Ser Gly Cys Glu Tyr Gln Gln Cys Pro Ser Glu		
500	505	510
Phe Asp Tyr Asn Ala Thr Asp His Ala Gly Lys Ser Ala Asn Glu		
515	520	525
Lys Ala Asp Ser Ala Gly Val Arg Pro Gly Ala Gln Ala Tyr Leu		
530	535	540
Leu Thr Val Phe Cys Ile Leu Phe Leu Val Met Gln Arg Glu Trp		
545	550	555

Arg

<210> 161
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 161
ctccgtggta aaccccacag ccc 23

<210> 162
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

卷之三

1 5 10 15
Leu Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg
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Gly His Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu
35 40 45
Gly Gly Gln Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro
50 55 60
Arg Arg Lys Phe Met Thr Val Ser Gly Leu Pro Lys Lys Gln Cys
65 70 75
Pro Cys Asp His Phe Lys Gly Asn Val Lys Lys Thr Arg His Gln
80 85 90
Arg His His Arg Lys Pro Asn Lys His Ser Arg Ala Cys Gln Gln
95 100 105
Phe Leu Lys Gln Cys Gln Leu Arg Ser Phe Ala Leu Pro Leu
110 115

<210> 166
<211> 551
<212> DNA
<213> Homo sapiens

<400> 166
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ccagacgact cgggcaaaga cccaaagcca gactttccca aattcctaag 150
cctcctggc acagagatca ttgagaatgc agtcgagttc atcctccgct 200
ccatgtccag gagcacagga ttatgaaat ttgatgataa tgaaggaaaa 250
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a 551

<210> 167
<211> 87
<212> PRT
<213> Homo sapiens

<400> 167
Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu
1 5 10 15
Val Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro

20

25

30

Asp Asp Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe
35 40 45
Pro Lys Phe Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala
50 55 60
Val Glu Phe Ile Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met
65 70 75
Glu Phe Asp Asp Asn Glu Gly Lys His Ser Ser Lys
80 85

<210> 168

<211> 1371

<212> DNA

<213> Homo sapiens

<400> 168
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ggaaggcagac ctcagagctg gtctgcattt gacatccgtt tcccactct 100
gcagctgtctt gtgtgtttt ttaccctgcc cctgcaccc atggctctgc 150
tgggctgtctt gcagccccctt tgcaaaagctt acttcccccta cctgtatggcc 200
gtgtgtactt ccaagagcaa ccgcaggatg gagaggaa aacggggact 250
cttcagccaggataaaaggggc ttacaggaggc ctccggggaa gtggccctac 300
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gcctcccaat gttgtccctt tccttcgttc ccatggtaaa gtcctctcg 1150
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tcatggtgcc tgcattccctg ccaagccccctgaccctct ctcggacta 1250
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atgccagago aagactcaaa gaggcagagg ttttgttctc aaatatttt 1350
taataaatag acgaaaccac g 1371

<210> 169
<211> 277
<212> PRT
<213> Homo sapiens

<400> 169
Met Asp Ile Leu Val Pro Leu Leu Gln Leu Leu Val Leu Leu Leu
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Thr Leu Pro Leu His Leu Met Ala Leu Leu Gly Cys Trp Gln Pro
20 25 30
Leu Cys Lys Ser Tyr Phe Pro Tyr Leu Met Ala Val Leu Thr Pro
35 40 45
Lys Ser Asn Arg Lys Met Glu Ser Lys Lys Arg Glu Leu Phe Ser
50 55 60
Gln Ile Lys Gly Leu Thr Gly Ala Ser Gly Lys Val Ala Leu Leu
65 70 75
Glu Leu Gly Cys Gly Thr Gly Ala Asn Phe Gln Phe Tyr Pro Pro
80 85 90 95
Gly Cys Arg Val Thr Cys Leu Asp Pro Asn Pro His Phe Glu Lys
95 100 105
Phe Leu Thr Lys Ser Met Ala Glu Asn Arg His Leu Gln Tyr Glu
110 115 120
Arg Phe Val Val Ala Pro Gly Glu Asp Met Arg Gln Leu Ala Asp
125 130 135
Gly Ser Met Asp Val Val Val Cys Thr Leu Val Leu Cys Ser Val
140 145 150
Gln Ser Pro Arg Lys Val Leu Gln Glu Val Arg Arg Val Leu Arg
155 160 165
Pro Gly Gly Val Leu Phe Phe Trp Glu His Val Ala Glu Pro Tyr
170 175 180
Gly Ser Trp Ala Phe Met Trp Gln Gln Val Phe Glu Pro Thr Trp
185 190 195
Lys His Ile Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr Trp Lys
200 205 210
Asp Leu Glu Asn Ala Gln Phe Ser Glu Ile Gln Met Glu Arg Gln
215 220 225

Pro Pro Pro Leu Lys Trp Leu Pro Val Gly Pro His Ile Met Gly
230 235 240
Lys Ala Val Lys Gln Ser Phe Pro Ser Ser Lys Ala Leu Ile Cys
245 250 255
Ser Phe Pro Ser Leu Gln Leu Glu Gln Ala Thr His Gln Pro Ile
260 265 270
Tyr Leu Pro Leu Arg Gly Thr
275

<210> 170
<211> 1621
<212> DNA
<213> Homo sapiens

<400> 170
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agcttctgttata gataagggtt aaaaactaat atttatatgtt cagaagaaaa 150
agatgtcattt ccgtaaagttt aacatcatca tcttggtcctt ggctgttgct 200
ctcttcttac ttgggttttttttccca ccataacttc ctcagcttgcgc 250
aaggaaatgtt gttacagattt caggaattgtt agggcctcaa cctatagact 300
ttgtccccaaat tgctctccga catgcgtttttt atggggagaca agaggagattt 350
cctgtggcata tcgcgtgcata tgaagacagg ctgggggggg ccattgcgc 400
tataaacagttt attcagcaca acactcgctt caatgttgcattt ttctacattt 450
ttactctcaaa caatacagca gaccatctcc ggtccctggctt caacagtgtt 500
tccctgaaaaaa gcatcagata caaaattgtt aattttgacc ctaaaactttt 550
ggaaggaaaaaa gttaaaggagg atccttgacc gggggaaatcc atgaaaccc 600
taacctttgc aagggttctatcc ttggccattt tggttcccaatcc cgaaagaag 650
gccatataca tggatgtatcc tgtaattgtt caaggtgtt ttcttgcctt 700
ttacaataca gcactgttttttgc caggacatgc agctgcattt tcagaagattt 750
gtgattcagttt ctctactaaa gttgtcatcc gtggagcagg aaaccaggatc 800
aattacattt gctatcttgc ctataaaaaaa gaaagaatttgc gtaagcttc 850
catggaaagcc agcacttgcattt cattttatcc tggagttttt gttgcaacc 900
tgacggaaatg gaaacgacac aataataactt accaactggaa aaaatggatg 950
aaactcaatg tagaaaggagg actgtatagc agaaccctgg ctggtagcat 1000
cacaacacctt cctctgttta tcgtatTTTA tcaacagcac tctaccatcg 1050
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tcacaccttgcgtt ttgttaaaggc tgccaaatgtt ccattttggaa atggacattt 1150

gaagccatgg ggaaggactg cttcatatac tcatgtttgg gaaaaatgg 1200
atattccaga cccaacaggc aaattcaacc taatccgaag atataccgag 1250
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aggaagtccct ggaagatagc atgcattggg agtaacagtt gctaggcttc 1350
aatgcctatc ggttagcaagc catggaaaaa gatgtgtcag ctaggtaaag 1400
atgacaaact gccctgtctg gcagtcagct tcccagacag actatagact 1450
ataaatatgt ctccatctgc cttaccaagt gttttcttac tacaatgtctg 1500
aatgactgga aagaagaact gatatggcta gttcagctag ctggtacaga 1550
taattcaaaa ctgctgttgg tttaatttt gtaacctgtg gcctgtatctg 1600
taaataaaaac ttacatcccc c 1621

<210> 171
<211> 371
<212> PRT
<213> Homo sapiens

<400> 171
Met Ser Phe Arg Lys Val Asn Ile Ile Ile Leu Val Leu Ala Val
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Ala Leu Phe Leu Leu Val Leu His His Asn Phe Leu Ser Leu Ser
20 25 30
Ser Leu Leu Arg Asn Glu Val Thr Asp Ser Gly Ile Val Gly Pro
35 40 45
Gln Pro Ile Asp Phe Val Pro Asn Ala Leu Arg His Ala Val Asp
50 55 60
Gly Arg Gln Glu Glu Ile Pro Val Val Ile Ala Ala Ser Glu Asp
65 70 75
Arg Leu Gly Gly Ala Ile Ala Ala Ile Asn Ser Ile Gln His Asn
80 85 90
Thr Arg Ser Asn Val Ile Phe Tyr Ile Val Thr Leu Asn Asn Thr
95 100 105
Ala Asp His Leu Arg Ser Trp Leu Asn Ser Asp Ser Leu Lys Ser
110 115 120
Ile Arg Tyr Lys Ile Val Asn Phe Asp Pro Lys Leu Leu Glu Gly
125 130 135
Lys Val Lys Glu Asp Pro Asp Gln Gly Glu Ser Met Lys Pro Leu
140 145 150
Thr Phe Ala Arg Phe Tyr Leu Pro Ile Leu Val Pro Ser Ala Lys
155 160 165
Lys Ala Ile Tyr Met Asp Asp Asp Val Ile Val Gln Gly Asp Ile
170 175 180
Leu Ala Leu Tyr Asn Thr Ala Leu Lys Pro Gly His Ala Ala Ala

185 190 195

Phe	Ser	Glu	Asp	Cys	Asp	Ser	Ala	Ser	Thr	Lys	Val	Val	Ile	Arg
200									205				210	
Gly	Ala	Gly	Asn	Gln	Tyr	Asn	Tyr	Ile	Gly	Tyr	Leu	Asp	Tyr	Lys
215									220				225	
Lys	Glu	Arg	Ile	Arg	Lys	Leu	Ser	Met	Lys	Ala	Ser	Thr	Cys	Ser
230									235				240	
Phe	Asn	Pro	Gly	Val	Phe	Val	Ala	Asn	Leu	Thr	Glu	Trp	Lys	Arg
245									250				255	
Gln	Asn	Ile	Thr	Asn	Gln	Leu	Glu	Lys	Trp	Met	Lys	Leu	Asn	Val
260									265				270	
Glu	Glu	Gly	Leu	Tyr	Ser	Arg	Thr	Leu	Ala	Gly	Ser	Ile	Thr	Thr
275									280				285	
Pro	Pro	Leu	Leu	Ile	Val	Phe	Tyr	Gln	Gln	His	Ser	Thr	Ile	Asp
290									295				300	
Pro	Met	Trp	Asn	Val	Arg	His	Leu	Gly	Ser	Ser	Ala	Gly	Lys	Arg
305									310				315	
Tyr	Ser	Pro	Gln	Phe	Val	Lys	Ala	Ala	Lys	Leu	Leu	His	Trp	Asn
320									325				330	
Gly	His	Leu	Lys	Pro	Trp	Gly	Arg	Thr	Ala	Ser	Tyr	Thr	Asp	Val
335									340				345	
Trp	Glu	Lys	Trp	Tyr	Ile	Pro	Asp	Pro	Thr	Gly	Lys	Phe	Asn	Leu
350									355				360	
Ile	Arg	Arg	Tyr	Thr	Glu	Ile	Ser	Asn	Ile	Lys				
					365					370				

<210> 172

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 71, 76, 86, 91, 162, 220, 269, 281

<223> unknown base

<400> 172

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aatgttctcc gacatgcagt agatgggaga caagaggaga ttccctgtgg 150
catcgctgc tntgaagaca ggcttgggggg ggccatttgca gctataaaca 200
gcatttcagca caaacactcgn tccaatgtga ttttctacat tgttactctc 250
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aagcatcaga tacaaaattt tcaatttttgc ccctaaactt ttggaaaggaa 350
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aagtaaagga ggatcctgac cagggggaat ocatgaaacc tttaacctt 400
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cagcactgaa gccaggacat gcagtcgtat tttcagaaga ttgtgattca 550
gcctctacta aagttgtcat ccgtggagca gaaaa 585

<210> 173
<211> 1866
<212> DNA
<213> Homo sapiens

<400> 173
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aacgcggggc gccagacaac gggctgggtt cccggccctg cggcgcgggc 150
gctgagctgg caggcgccgtt cggggcgccg gctgcatccg catctccccc 200
atcgccctgca gtaaggccgg cccggccgag ctttgaggg gaacgacttg 250
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tcacatcaact ttccgatcac ttcaaagtgg ttaaaaacta atatttatat 350
gacagaagaa aaagatgtca ttccgtaaag taaacatcat catctggtc 400
ctgggctgtt gctctcttct tactgtttt gcaccataac ttccctcgat 450
tgaggcagt tggtaaggaa tgaggataca gattcagga tttagggcc 500
tcacacctata ggactttgtc ccaaattgtc tccgacatgc agtagatggg 550
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ggggggccattt gcagctataa acagcattca gcacaacact cgctccaaatg 650
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tgggctcaac agtgattttcc tggaaagcat cagataaaaa attgtcaatt 750
ttgaccctaa acttttgaa ggaaaagtaa aggaggatcc tgaccagggg 800
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aactggaaaa atggatgaaa ctcaatgttag aagaggact gtatagcaga 1200

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tttcttacta caatgctgaa tgactggaaa gaagaactga tatggctagt 1750
tcagctagct ggtacagata attcaaaact gctgtgggtt ttaattttgt 1800
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aaaaaaaaaaa aaaaaa 1866

<210> 174
<211> 823
<212> DNA
<213> Homo sapiens

<400> 174
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ctcaccattt aggcagctcc actgtctgtg ctggctctgat ggtgctgcct 150
gtcatggggg cagccatctc ccagggggcc ctcatgccta tcgtctgcaa 200
cggtctctgtt ggcttcttc tgctgctgtc ctgggtcata ctctgctggg 250
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actccagcccc tggccctgtt cctgagaagg cccaccacc ccagaagccc 350
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cagatctcag ccagcctggg gtccagaactt caagagtccg cctgcttgaa 500
gtctggccatc gcccggcaga gtctagccat cttggctccat ataggagctc 550
atgtggccata aggatgtgg cctgggggtgg gggctttaga gttgggtgcta 600
gagccaggcc catctggact atgctccatc ccaaggccca agggtcagg 650
gcccgggttcca ctctttccctt aggctgacca cctcttaggcc ctcttaggtt 700
ggaaagcaaa ctggaaaccca tggcaataat aggagggtgtt ccaggctggg 750

ccctccccct ggtcctccca gtgttgctg gataataat ggaactatgg 800
ctctaaaaaa aaaaaaaaaaaa aaa 823

<210> 175
<211> 87
<212> PRT
<213> Homo sapiens

<400> 175
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1 5 10 15
Asn Gly Leu Val Gly Phe Leu Leu Leu Leu Trp Val Ile Leu
20 25 30
Cys Trp Ala Cys His Ser Arg Leu Pro Thr Leu Thr Leu Ser Leu
35 40 45
Asn Pro Val Pro Thr Pro Ala Leu Ala Pro Val Leu Arg Arg Pro
50 55 60
His His Pro Arg Ser Pro Ala Met Lys Ala Ala Thr Cys Cys Ser
65 70 75
Pro Glu Gly Pro Trp Pro Ser Leu Glu Pro Arg Thr
80 85

<210> 176
<211> 1660
<212> DNA
<213> Homo sapiens

<400> 176
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cccgaggctac cagttctcc aagcaagtca tttcccttat ttaaccgatg 100
tgtccctcaa acacctgagt gctactccct attgcacatc gttttgataa 150
atatgttta caccctccac cgaattctaa gtggaatcat gtccggaga 200
gataacaatcc ttggcctgt tatcctgcga ttagcctgt ctggccat 250
gtatgttacc ttcaagatca tcaccaccct tctggatcac attttcattt 300
catggttat ttgggattt ttgtttgtct gcgggtttt atggggctg 350
tattatgact ataccaacga cctcagcata gaattggaca cagaaaggga 400
aaatatgaag tgcggtcg 450
cagtgctgctc cgttttgcatttttca gaaagagaat aaatttgcata 500
gttggatcc 550
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gtggatcgatc catttaattt gcctcatctg gactgtgaa ttcatccctt 750

卷之三

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<212> PRT
<213> *Homo sapiens*

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Leu Leu Val His Ile Phe Ile Ser Leu Val Ile Leu Gly Leu Leu
      35                     40                     45
Phe Val Cys Gly Val Leu Trp Trp Leu Tyr Tyr Asp Tyr Thr Asn
      50                     55                     60
Asp Leu Ser Ile Glu Leu Asp Thr Glu Arg Glu Asn Met Lys Cys
      65                     70                     75
Val Leu Gly Phe Ala Ile Val Ser Thr Gly Ile Thr Ala Val Leu
      80                     85                     90
Leu Val Leu Ile Phe Val Leu Arg Lys Arg Ile Lys Leu Thr Val

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Glu Leu Phe Gln Ile Thr Asn Lys Ala Ile Ser Ser Ala Pro Phe		
110	115	120
Leu Leu Phe Gln Pro Leu Trp Thr Phe Ala Ile Leu Ile Phe Phe		
125	130	135
Trp Val Leu Trp Val Ala Val Leu Leu Ser Leu Gly Thr Ala Gly		
140	145	150
Ala Ala Gln Val Met Glu Gly Gly Gln Val Glu Tyr Lys Pro Leu		
155	160	165
Ser Gly Ile Arg Tyr Met Trp Ser Tyr His Leu Ile Gly Leu Ile		
170	175	180
Trp Thr Ser Glu Phe Ile Leu Ala Cys Gln Gln Met Thr Ile Ala		
185	190	195
Gly Ala Val Val Thr Cys Tyr Phe Asn Arg Ser Lys Asn Asp Pro		
200	205	210
Pro Asp His Pro Ile Leu Ser Ser Leu Ser Ile Leu Phe Phe Tyr		
215	220	225
His Gln Gly Thr Val Val Lys Gly Ser Phe Leu Ile Ser Val Val		
230	235	240
Arg Ile Pro Arg Ile Ile Val Met Tyr Met Gln Asn Ala Leu Lys		
245	250	255
Glu Gln Gln His Gly Ala Leu Ser Arg Tyr Leu Phe Arg Cys Cys		
260	265	270
Tyr Cys Cys Phe Trp Cys Leu Asp Lys Tyr Leu Leu His Leu Asn		
275	280	285
Gln Asn Ala Tyr Thr Thr Ala Ile Asn Gly Thr Asp Phe Cys		
290	295	300
Thr Ser Ala Lys Asp Ala Phe Lys Ile Leu Ser Lys Asn Ser Ser		
305	310	315
His Phe Thr Ser Ile Asn Cys Phe Gly Asp Phe Ile Ile Phe Leu		
320	325	330
Gly Lys Val Leu Val Val Cys Phe Thr Val Phe Gly Gly Leu Met		
335	340	345
Ala Phe Asn Tyr Asn Arg Ala Phe Gln Val Trp Ala Val Pro Leu		
350	355	360
Leu Leu Val Ala Phe Phe Ala Tyr Leu Val Ala His Ser Phe Leu		
365	370	375
Ser Val Phe Glu Thr Val Leu Asp Ala Leu Phe Leu Cys Phe Ala		
380	385	390
Val Asp Leu Glu Thr Asn Asp Gly Ser Ser Glu Lys Pro Tyr Phe		
395	400	405
Met Asp Gln Glu Phe Leu Ser Phe Val Lys Arg Ser Asn Lys Leu		

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<211> 2773
<212> DNA
<213> Homo sapiens

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卷之三

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<211> 678
<212> PRT
<213> Homo sapiens

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Ala Lys Lys Ile Lys Arg Pro Lys Phe Thr Val Pro Gln Ile Asn
35 40 45
Cys Asp Val Lys Ala Gly Lys Ile Ile Asp Pro Glu Phe Ile Val
50 55 60
Lys Cys Pro Ala Gly Cys Gln Asp Pro Lys Tyr His Val Tyr Gly
65 70 75
Thr Asp Val Tyr Ala Ser Tyr Ser Ser Val Cys Gly Ala Ala Val
80 85 90
His Ser Gly Val Leu Asp Asn Ser Gly Gly Lys Ile Leu Val Arg
95 100 105
Lys Val Ala Gly Gln Ser Gly Tyr Lys Gly Ser Tyr Ser Asn Gly
110 115 120
Val Gln Ser Leu Ser Leu Pro Arg Trp Arg Glu Ser Phe Ile Val
125 130 135
Leu Glu Ser Lys Pro Lys Lys Gly Val Thr Tyr Pro Ser Ala Leu
140 145 150
Thr Tyr Ser Ser Lys Ser Pro Ala Ala Gln Ala Gly Glu Thr
155 160 165
Thr Lys Ala Tyr Gln Arg Pro Pro Ile Pro Gly Thr Thr Ala Gln
170 175 180
Pro Val Thr Leu Met Gln Leu Leu Ala Val Thr Val Ala Val Ala
185 190 195
Thr Pro Thr Thr Leu Pro Arg Pro Ser Pro Ser Ala Ala Ser Thr
200 205 210
Thr Ser Ile Pro Arg Pro Gln Ser Val Gly His Arg Ser Gln Glu
215 220 225
Met Asp Leu Trp Ser Thr Ala Thr Tyr Thr Ser Ser Gln Asn Arg
230 235 240
Pro Arg Ala Asp Pro Gly Ile Gln Arg Gln Asp Pro Ser Gly Ala
245 250 255
Ala Phe Gln Lys Pro Val Gly Ala Asp Val Ser Leu Gly Leu Val
260 265 270
Pro Lys Glu Glu Leu Ser Thr Gln Ser Leu Glu Pro Val Ser Leu
275 280 285
Gly Asp Pro Asn Cys Lys Ile Asp Leu Ser Phe Leu Ile Asp Gly

290	295	300
Ser Thr Ser Ile Gly Lys Arg Arg Phe Arg Ile Gln Lys Gln Leu		
305	310	315
Leu Ala Asp Val Ala Gln Ala Leu Asp Ile Gly Pro Ala Gly Pro		
320	325	330
Leu Met Gly Val Val Gln Tyr Gly Asp Asn Pro Ala Thr His Phe		
335	340	345
Asn Leu Lys Thr His Thr Asn Ser Arg Asp Leu Lys Thr Ala Ile		
350	355	360
Glu Lys Ile Thr Gln Arg Gly Gly Leu Ser Asn Val Gly Arg Ala		
365	370	375
Ile Ser Phe Val Thr Lys Asn Phe Phe Ser Lys Ala Asn Gly Asn		
380	385	390
Arg Ser Gly Ala Pro Asn Val Val Val Met Val Asp Gly Trp		
395	400	405
Pro Thr Asp Lys Val Glu Glu Ala Ser Arg Leu Ala Arg Glu Ser		
410	415	420
Gly Ile Asn Ile Phe Phe Ile Thr Ile Glu Gly Ala Ala Glu Asn		
425	430	435
Glu Lys Gln Tyr Val Val Glu Pro Asn Phe Ala Asn Lys Ala Val		
440	445	450
Cys Arg Thr Asn Gly Phe Tyr Ser Leu His Val Gln Ser Trp Phe		
455	460	465
Gly Leu His Lys Thr Leu Gln Pro Leu Val Lys Arg Val Cys Asp		
470	475	480
Thr Asp Arg Leu Ala Cys Ser Lys Thr Cys Leu Asn Ser Ala Asp		
485	490	495
Ile Gly Phe Val Ile Asp Gly Ser Ser Val Gly Thr Gly Asn		
500	505	510
Phe Arg Thr Val Leu Gln Phe Val Thr Asn Leu Thr Lys Glu Phe		
515	520	525
Glu Ile Ser Asp Thr Asp Thr Arg Ile Gly Ala Val Gln Tyr Thr		
530	535	540
Tyr Glu Gln Arg Leu Glu Phe Gly Phe Asp Lys Tyr Ser Ser Lys		
545	550	555
Pro Asp Ile Leu Asn Ala Ile Lys Arg Val Gly Tyr Trp Ser Gly		
560	565	570
Gly Thr Ser Thr Gly Ala Ala Ile Asn Phe Ala Leu Glu Gln Leu		
575	580	585
Phe Lys Lys Ser Lys Pro Asn Lys Arg Lys Leu Met Ile Leu Ile		
590	595	600
Thr Asp Gly Arg Ser Tyr Asp Asp Val Arg Ile Pro Ala Met Ala		

605	610	615
Ala His Leu Lys Gly Val Ile Thr Tyr Ala Ile Gly Val Ala Trp		
620	625	630
Ala Ala Gln Glu Glu Leu Glu Val Ile Ala Thr His Pro Ala Arg		
635	640	645
Asp His Ser Phe Phe Val Asp Glu Phe Asp Asn Leu His Gln Tyr		
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Val Pro Arg Ile Ile Gln Asn Ile Cys Thr Glu Phe Asn Ser Gln		
665	670	675

Pro Arg Asn

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<211> 1759
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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Asp Pro Ala His Tyr Ser Phe Ser Leu Thr Leu Ile Asp Ala Leu
35 40 45
Asp Thr Leu Leu Ile Leu Gly Asn Val Ser Glu Phe Gln Arg Val
50 55 60
Val Glu Val Leu Gln Asp Ser Val Asp Phe Asp Ile Asp Val Asn
65 70 75
Ala Ser Val Phe Glu Thr Asn Ile Arg Val Val Gly Gly Leu Leu
80 85 90
Ser Ala His Leu Leu Ser Lys Lys Ala Gly Val Glu Val Glu Ala
95 100 105
Gly Trp Pro Cys Ser Gly Pro Leu Leu Arg Met Ala Glu Glu Ala
110 115 120
Ala Arg Lys Leu Leu Pro Ala Phe Gln Thr Pro Thr Gly Met Pro

1994-1995-1996-1997

125

130

135

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Ala	Thr	Leu	Ser	Ser	Leu	Thr	Gly	Asp	Pro	Val	Phe	Glu	Asp	Val
			170						175					180
Ala	Arg	Val	Ala	Leu	Met	Arg	Leu	Trp	Glu	Ser	Arg	Ser	Asp	Ile
			185						190					195
Gly	Leu	Val	Gly	Asn	His	Ile	Asp	Val	Leu	Thr	Gly	Lys	Trp	Val
			200						205					210
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Tyr	Leu	Val	Lys	Gly	Ala	Ile	Leu	Leu	Gln	Asp	Lys	Lys	Leu	Met
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Ala	Met	Phe	Leu	Glu	Tyr	Asn	Lys	Ala	Ile	Arg	Asn	Tyr	Thr	Arg
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Phe	Asp	Asp	Trp	Tyr	Leu	Trp	Val	Gln	Met	Tyr	Lys	Gly	Thr	Val
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Ser	Met	Pro	Val	Phe	Gln	Ser	Leu	Glu	Ala	Tyr	Trp	Pro	Gly	Leu
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Gln	Ser	Leu	Ile	Gly	Asp	Ile	Asp	Asn	Ala	Met	Arg	Thr	Phe	Leu
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Asn	Tyr	Tyr	Thr	Val	Trp	Lys	Gln	Phe	Gly	Gly	Leu	Pro	Glu	Phe
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Tyr	Asn	Ile	Pro	Gln	Gly	Tyr	Thr	Val	Glu	Lys	Arg	Glu	Gly	Tyr
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Pro	Leu	Arg	Pro	Glu	Leu	Ile	Glu	Ser	Ala	Met	Tyr	Leu	Tyr	Arg
			335						340					345
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Glu	Ser	Ile	Glu	Lys	Ile	Ser	Lys	Val	Glu	Cys	Gly	Phe	Ala	Thr
			365						370					375
Ile	Lys	Asp	Leu	Arg	Asp	His	Lys	Leu	Asp	Asn	Arg	Met	Glu	Ser
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Phe	Phe	Leu	Ala	Glu	Thr	Val	Lys	Tyr	Leu	Tyr	Leu	Phe	Asp	
			395						400					405
Pro	Thr	Asn	Phe	Ile	His	Asn	Asn	Gly	Ser	Thr	Phe	Asp	Ala	Val
			410						415					420
Ile	Thr	Pro	Tyr	Gly	Glu	Cys	Ile	Leu	Gly	Ala	Gly	Gly	Tyr	Ile
			425						430					435
Phe	Asn	Thr	Glu	Ala	His	Pro	Ile	Asp	Leu	Ala	Ala	Leu	His	Cys

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Cys Gln Arg Leu Lys Glu Glu Gln Trp Glu Val Glu Asp Leu Met
455 460 465
Arg Glu Phe Tyr Ser Leu Lys Arg Ser Arg Ser Lys Phe Gln Lys
470 475 480
Asn Thr Val Ser Ser Gly Pro Trp Glu Pro Pro Ala Arg Pro Gly
485 490 495
Thr Leu Phe Ser Pro Glu Asn His Asp Gln Ala Arg Glu Arg Lys
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Pro Ala Lys Gln Lys Val Pro Leu Leu Ser Cys Pro Ser Gln Pro
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<211> 2056
<212> DNA
<213> Homo sapiens

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acggaggatc catgaactac tgtaaagtgt tgacagtgt tgcacactgc 1900
agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
gtaacatgtt catgtttgtt gtgtccctt tttctgttgg taaagtacag 2000
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aaaaaa 2056

<210> 183
<211> 311
<212> PRT
<213> Homo sapiens

<220>
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<222> 1-29
<223> Signal peptide

<220>
<221> N-glycosylation sites
<222> 40-43, 134-137

<223> N-glycosylation sites.

<220>
<221> Tissue factor proteins homology
<222> 92-119
<223> Tissue factor proteins homology

<220>
<221> Transmembrane domain
<222> 230-255
<223> Transmembrane domain

<220>
<221> Integrins alpha chain protein homology
<222> 232-262
<223> Integrins alpha chain protein homology

<400> 183
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Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp
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Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
35 40 45
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro
50 55 60
Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu
65 70 75
Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser
80 85 90
Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala
95 100 105
Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln
110 115 120
Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser
125 130 135
Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe
140 145 150
His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe
155 160 165
Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val
170 175 180
Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met
185 190 195
Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys
200 205 210
Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu
215 220 225

Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
 230 235 240
 Val Gly Phe Met Leu Ile Leu Val Val Pro Leu Phe Val Trp
 245 250 255
 Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val
 260 265 270
 Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
 275 280 285
 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met
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 Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
 305 310

<210> 184
 <211> 808
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 654, 711, 748
 <223> unknown base

<400> 184
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 tagaccttcag ctccaaacata tgcatcttg agaaaagatgg ctgagatgac 150
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 ccaaattgcag actttcacaa tggttctaga agaaaatctgg acaagtcttt 250
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 gcatcttttgc atgtggagcc cagtgttcgc gcctggagaa acagtgtact 400
 attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450
 tggatccccca gcagctggtg ctcacttc当地 gaaggctctg agtgtgtatgt 500
 cactgtatgc atcacggcca ctgtgccata caacctttgt gtcaggccca 550
 cattgggctc acagacccctca gcctggagca tccctgaagca tcccttaat 600
 agaaaactcaa ccaccccttac ccgacccctgg atggagatca ccaaagatgg 650
 cttnccacctg gtttattggc ttgaggaggct gggggccccag tttgagttcc 700
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
 gaacccttgc cggccgtgg ggtatctctc gagaaaaagag agggccaaata 800
 tgacccac 808

<210> 185
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
aggcttcgtc gcgactagac ctc 23

<210> 186
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
ccaggtcggg taaggatggt tgag 24

<210> 187
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tttctacgca ttgattccat gtttgctcac agatgaagtgc gccattctgc 50

<210> 188
<211> 1227
<212> DNA
<213> Homo sapiens

<400> 188
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ggcagcggcg tggctgtc tggggctgc ggcctgcgc cagcaggagc 100
aggacttcta cgacttcaag gggtaaca tccggggca actgggttcg 150
ctggagaagt acogcggatc ggtgtccctg gtggtaatg tggccagcga 200
gtgcggcttc acagaccagg actaccgagc cctgcagcag ctgcagcgg 250
acctgggccc ccaccactt aacgtgtcg cttccccctg caaccagg 300
ggccaacagg agcctgacag caacaaggag attgagagct ttgcccggc 350
cacctacagt gtctcattcc ccatgttagt caagattgca gtcacccgta 400
ctgggtggca tcctgccttc aagtacactgg cccagacttc tggaaaggag 450
cccacctggaa acttctggaa gtacctgatg gccccagatg gaaagggtgg 500
aggggcttgg gacccaaactg tgcgtggaa ggaggtcaga cccagatca 550
cagcgcgtt gaggaaagctc atccctactga agcgagaaga cttataacca 600

TOP SECRET

ccgcgtctcc tcctccacca cctcatcccg cccacctgtg tggggctgac 650
caatgaaac tcaaattgggt cttaaaaggag agagaccac tgactctct 700
tcctttactc ttatgccatt ggtcccatca ttcttgggg gaaaaattc 750
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<210> 189

<211> 187

<212> PRT

<213> Homo sapiens

<400> 189

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Ala	Ala	Cys	Ala	Gln	Gln	Glu	Gln	Asp	Phe	Tyr	Asp	Phe	Lys	Ala
					20				25					30
Val	Asn	Ile	Arg	Gly	Lys	Leu	Val	Ser	Leu	Glu	Lys	Tyr	Arg	Gly
					35				40					45
Ser	Val	Ser	Leu	Val	Val	Asn	Val	Ala	Ser	Glu	Cys	Phe	Thr	
					50				55					60
Asp	Gln	His	Tyr	Arg	Ala	Leu	Gln	Gln	Leu	Gln	Arg	Asp	Leu	Gly
					65				70					75
Pro	His	His	Phe	Asn	Val	Leu	Ala	Phe	Pro	Cys	Asn	Gln	Phe	Gly
					80				85					90
Gln	Gln	Glu	Pro	Asp	Ser	Asn	Lys	Glu	Ile	Glu	Ser	Phe	Ala	Arg
					95				100					105
Arg	Thr	Tyr	Ser	Val	Ser	Phe	Pro	Met	Phe	Ser	Lys	Ile	Ala	Val
					110				115					120
Thr	Gly	Thr	Gly	Ala	His	Pro	Ala	Phe	Lys	Tyr	Leu	Ala	Gln	Thr
					125				130					135
Ser	Gly	Lys	Glu	Pro	Thr	Trp	Asn	Phe	Trp	Lys	Tyr	Leu	Val	Ala
					140				145					150
Pro	Asp	Gly	Lys	Val	Val	Gly	Ala	Trp	Asp	Pro	Thr	Val	Ser	Val

155

160

165

Glu Glu Val Arg Pro Gln Ile Thr Ala Leu Val Arg Lys Leu Ile
170 175 180

Leu Leu Lys Arg Glu Asp Leu
185

<210> 190

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 190

gcaggacttc tacgacttca aggc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 191

agtctgggcc aggtacttga aggc 24

<210> 192

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 192

caacatccgg ggaaactgg tgcgcgtgg aaagtaccgc ggatcggtgt 50

<210> 193

<211> 2187

<212> DNA

<213> Homo sapiens

<400> 193

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ctggggggccc gggccgcctt ctctcggtt tggcaggaa ccagggttgc 150

gggtgtccgc ttccctcgtt ccagagagg gtatcgcatg gtctccacgc 200

ccatcgaggc cctcagctac gttcagggtt gcacaaaaa gcatcttaac 250

agcaagactg tggccgttgc cctggagacc acagcacaga gggtcccaga 300

acgagaggcc ttggctgtcc tccatgaaga cgtcagggtt acctttgcc 350

aactcaagga ggagggtggac aaagctgtt ctggcctcct gaggattggc 400

ctctgcaaag gtgaccggct gggcatgtgg ggacctaact cctatgcatt 450
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agctgaacacgcggggggatgtgtcatcc gagggtactgcgtcatgt 1450
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aacttcgaga gcagatggaa cgacatctaa atctgtgaat aaagcagcag 1850
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aatgtcaagg aattgactga acgaactaag agtccttgg agggtccggg 2050
aactcgctg ggcacaaggc gccaaaaggc aggccgcctg cccaggccct 2100
ccctcctgtc catccccac attccctgt ctgtccttgt gatttggcat 2150
aaagagcttc tgttttcttt gaaaaaaaaaaaaaa 2187

<210> 194
<211> 615
<212> PRT
<213> Homo sapiens

<400> 194
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Gly Ser Ser Gly Val Leu Gly Ala Arg Ala Ala Leu Ser Arg Ser
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Trp Gln Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg
35 40 45
Glu Val Asp Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr
50 55 60
Val Gln Gly Cys Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly
65 70 75
Gln Cys Leu Glu Thr Thr Ala Gln Arg Val Pro Glu Arg Glu Ala
80 85 90
Leu Val Val Leu His Glu Asp Val Arg Leu Thr Phe Ala Gln Leu
95 100 105
Lys Glu Glu Val Asp Lys Ala Ala Ser Gly Leu Leu Ser Ile Gly
110 115 120
Leu Cys Lys Gly Asp Arg Leu Gly Met Trp Gly Pro Asn Ser Tyr
125 130 135
Ala Trp Val Leu Met Gln Leu Ala Thr Ala Gln Ala Gly Ile Ile
140 145 150
Leu Val Ser Val Asn Pro Ala Tyr Gln Ala Met Glu Leu Glu Tyr
155 160 165
Val Leu Lys Lys Val Gly Cys Lys Ala Leu Val Phe Pro Lys Gln
170 175 180
Phe Lys Thr Gln Gln Tyr Tyr Asn Val Leu Lys Gln Ile Cys Pro
185 190 195
Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln Arg Leu
200 205 210
Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro Gly
215 220 225
Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln
230 235 240
His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His

PDB ID: 1D9D

	245	250	255
Asp Pro Ile Asn Ile Gln Phe Thr Ser Gly Thr Thr Gly Ser Pro	260	265	270
Lys Gly Ala Thr Leu Ser His Tyr Asn Ile Val Asn Asn Ser Asn	275	280	285
Ile Leu Gly Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu Gln	290	295	300
Leu Arg Met Ile Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser	305	310	315
Val Ala Gly Thr Met Met Cys Leu Met Tyr Gly Ala Thr Leu Ile	320	325	330
Leu Ala Ser Pro Ile Phe Asn Gly Lys Lys Ala Leu Glu Ala Ile	335	340	345
Ser Arg Glu Arg Gly Thr Phe Leu Tyr Gly Thr Pro Thr Met Phe	350	355	360
Val Asp Ile Leu Asn Gln Pro Asp Phe Ser Ser Tyr Asp Ile Ser	365	370	375
Thr Met Cys Gly Gly Val Ile Ala Gly Ser Pro Ala Pro Pro Glu	380	385	390
Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn Met Lys Asp Leu Val	395	400	405
Val Ala Tyr Gly Thr Thr Glu Asn Ser Pro Val Thr Phe Ala His	410	415	420
Phe Pro Glu Asp Thr Val Glu Gln Lys Ala Glu Ser Val Gly Arg	425	430	435
Ile Met Pro His Thr Glu Ala Arg Ile Met Asn Met Glu Ala Gly	440	445	450
Thr Leu Ala Lys Leu Asn Thr Pro Gly Glu Leu Cys Ile Arg Gly	455	460	465
Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu Pro Gln Lys Thr Glu	470	475	480
Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr Gly Asp Val Ala	485	490	495
Thr Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly Arg Ser Lys	500	505	510
Asp Met Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala Glu Leu	515	520	525
Glu Asp Phe Phe His Thr His Pro Lys Val Gln Glu Val Gln Val	530	535	540
Val Gly Val Lys Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys	545	550	555
Ile Arg Leu Lys Asp Gly Glu Glu Thr Thr Val Glu Glu Ile Lys			

560	565	570
Ala Phe Cys Lys Gly Lys Ile Ser His Phe Lys Ile Pro Lys Tyr		
575 .	580	585
Ile Val Phe Val Thr Asn Tyr Pro Leu Thr Ile Ser Gly Lys Ile		
590	595	600
Gln Lys Phe Lys Leu Arg Glu Gln Met Glu Arg His Leu Asn Leu		
605	610	615

<210> 195
<211> 642
<212> DNA
<213> *Homo sapiens*

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gaggcacctt cctgtatgtt acccccacga tgttctgttga cattctgtac 250
cagccgacact tctccaggtt tgacatctcg accatgtgtg gaggtgtcat 300
tgtgggtcc cctgacccctc cagagtgtat ccgagccatc atcaacaaga 350
taaatatgaa ggacctggtg gttgtttatg gaaccacaga gaacagtccc 400
gtgacattcg cgcaacttccc tgaggacact gtggggcaga aggccaaaa 450
cgtggcaga attatgcctc acacggggc gggatcatg aacatgggg 500
cagggacgct ggcaaagctg aacacgcccc gggagctgtg catccgagg 550
tactgcgtca tgctgggtca ctggggtagt cctcagaaga cagaggaa 600
atggatcatg gacaatgtt attggacagg agatgtcccc ac 642
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<210> 196
<211> 1575
<212> DNA
<213> *Homo sapiens*

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<400> 196  
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aggccctgga gtgctacaga tgcgtgcaga aagcagatga cggatgcctc 150  
ccgaacaaga tgaagacagt gaagtgcgcg ccgggcgtgg acgtctgcac 200  
cgaggccgtg gggggcgtgg agaccatcca cggacaattc tcgctggcag 250  
tgcggggttt cggttcggga ctccccggca agaatgaccg cggcctggat 300  
cttacgggc ttcttggcatt catccaaqtq caqcaatgcg ctcaggatcg 350
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ctgcaacgcc aagctcaacc tcacctcgcg ggcgctcgac ccggcaggta 400
atgagagtgc atacccgccc aacggcggtg agtgctacag ctgtgtggc 450
ctgagccggg aggcgtgcca gggtacatcg cgcccggtcg tgagctgcta 500
caacgccagc gatcatgtct acaagggtcg cttcgacggc aacgtcacct 550
tgacggcagc taatgtact gtgtcctgc ctgtccggg ctgtgtccag 600
gatgaattct gcactcgaaa tggagtaaca gccccagggt tcacgctcag 650
tggctctgt tgccagggtt cccgctgtaa ctctgaccc tcgacaacaaga 700
cctacttctc ccttcgaatc ccaccccttg tccggctgcc ccctccagag 750
ccccacgactg tggcctcaac cacatgtgc accacttcta cctcgcccc 800
agtgagaccc acatccacca ccaaaccat gccagcgcca accagtcaaga 850
ctccgagaca gggagtagaa cacgaggctt cccggatga ggagccagg 900
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<210> 197

<211> 346

<212> PRT

<213> Homo sapiens

<400> 197

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Ala	Gly	Trp	Leu	Leu	Leu	Leu	Leu	Arg	Gly	Gly	Ala	Gln	Ala	
														30

Leu Glu Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser

35	40	45
Pro Asn Lys Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val		
50	55	60
Cys Thr Glu Ala Val Gly Ala Val Glu Thr Ile His Gly Gln Phe		
65	70	75
Ser Leu Ala Val Arg Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn		
80	85	90
Asp Arg Gly Leu Asp Leu His Gly Leu Leu Ala Phe Ile Gln Leu		
95	100	105
Gln Gln Cys Ala Gln Asp Arg Cys Asn Ala Lys Leu Asn Leu Thr		
110	115	120
Ser Arg Ala Leu Asp Pro Ala Gly Asn Glu Ser Ala Tyr Pro Pro		
125	130	135
Asn Gly Val Glu Cys Tyr Ser Cys Val Gly Leu Ser Arg Glu Ala		
140	145	150
Cys Gln Gly Thr Ser Pro Pro Val Val Ser Cys Tyr Asn Ala Ser		
155	160	165
Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn Val Thr Leu Thr		
170	175	180
Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly Cys Val Gln		
185	190	195
Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly Phe Thr		
200	205	210
Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg Cys Asn Ser Asp Leu		
215	220	225
Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile Pro Pro Leu Val Arg		
230	235	240
Leu Pro Pro Pro Glu Pro Thr Thr Val Ala Ser Thr Thr Ser Val		
245	250	255
Thr Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys		
260	265	270
Pro Met Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu		
275	280	285
His Glu Ala Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala		
290	295	300
Ala Gly His Gln Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys		
305	310	315
Gly Gly Pro Gln Gln Pro His Asn Lys Gly Cys Val Ala Pro Thr		
320	325	330
Ala Gly Leu Ala Ala Leu Leu Leu Ala Val Ala Ala Gly Val Leu		
335	340	345
Leu		

<210> 198
<211> 1657
<212> DNA
<213> Homo sapiens

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gtcctggcca gtgcagctg aaaggagaag gaaatggacc cttttcatta 150
tgattaccag accctgagga ttggggact ggtgttcgt gtggctct 200
tctcggttgg gatcctctt atccctaagtgc gcaggtgcaaa gtgcagttc 250
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<210> 199
<211> 120
<212> PRT
<213> Homo sapiens

<400> 199
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Val Leu Ala Ser Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe
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His Tyr Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu Val Phe Ala
35 40 45
Val Val Leu Phe Ser Val Gly Ile Leu Leu Ile Leu Ser Arg Arg
50 55 60
Cys Lys Cys Ser Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp Glu
65 70 75
Glu Ala Gln Val Glu Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro
80 85 90
Gln Lys Gln Arg Thr Glu Val Gln Pro Ser Gly Gly Ser Leu Trp
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Asn Leu Arg Arg Leu Leu Glu Pro Leu Asp Ala Asn Val Asp Ala
110 115 120

<210> 200
<211> 415
<212> DNA
<213> Homo sapiens

<400> 200
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ccgttccctga acatcgacaa attgcgtatc gcgttaagg ctgtatgagg 200
cctgaactgg cacggccctt ttgagtctat caaaaggaaa cttcccttcc 250
tcaactggaa tgccttccat aagctgaaag gactgaggag cgcaactcc 300
gatccccatc gaccatgacc tccactggaa gagggggcta gcgtgagcgc 350
tgattctcaa cctaccataa ctcttctgt cctcaggAAC tccaataaaa 400

cattttccat caaaa 415
<210> 201
<211> 99
<212> PRT
<213> Homo sapiens
<400> 201
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1 5 10 15
Val Leu His Ser Ala Gln Gly Ala Thr Leu Gly Gly Pro Glu Glu
20 25 30
Glu Ser Thr Ile Glu Asn Tyr Ala Ser Arg Pro Glu Ala Phe Asn
35 40 45
Thr Pro Phe Leu Asn Ile Asp Lys Leu Arg Ser Ala Phe Lys Ala
50 55 60
Asp Glu Phe Leu Asn Trp His Ala Leu Phe Glu Ser Ile Lys Arg
65 70 75
Lys Leu Pro Phe Leu Asn Trp Asp Ala Phe Pro Lys Leu Lys Gly
80 85 90
Leu Arg Ser Ala Thr Pro Asp Ala Gln
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<210> 202
<211> 678
<212> DNA
<213> Homo sapiens
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cagcaggagt ctcccaggtt gttttctcc agccagttc aactcaggag 150
acaggccca aggcatggg agatctctc tggcgcttg cggccactc 200
atgagagtgt ttttgttcaa agtattttt agaataactgt tgacttctc 250
atgatttaat aaccatctt tgcaaggtt tatgaggctt tagggaaatg 300
tcaaccctca aatttttgtt atactagatg gcttccattt acccaccact 350
attttaaggt ccctttattt ttaggttcaa ggttcattt acttgagaaa 400
gtgccttct gcagttcat tgattttgtt tatettcaat attaattgtt 450
acgattaaaa aagaataaga gcacgcagac ctctaggaga atattttatc 500
cctgggtgcc cctgacacat ttatgttagtg atccccacaa tgtgattgtt 550
aattttaatg ttatttcaat attagtatcat tcagttgtt tgtaatatgt 600
ataaccagaa tctattttt aaaaagggtttt agtatatttt tcaactagat 650
atttgatag aagactgaa tagtgtatg 678

<210> 203
<211> 52
<212> PRT
<213> Homo sapiens

<400> 203
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Ser Leu Leu Ala Ala Gly Val Ser Gln Val Val Leu Leu Gln Pro
20 25 30
Val Pro Thr Gln Glu Thr Gly Pro Lys Ala Met Gly Asp Leu Ser
35 40 45
Cys Gly Phe Ala Gly His Ser
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<210> 204
<211> 1917
<212> DNA
<213> Homo sapiens

<400> 204
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agaaggagtc aggttcaaaa tggaaaggat ttattgacca aattaacagg 150
tctttggaga attacgaacc atgttcaagt caaaactgc gctgctacca 200
tggtgtcata gaagaggatc taactccccc ccggaggaggc atctccagg 250
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caatttatcc tacaggatctt ggacgggtgg accttccatc agaagatctg 600
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tacaatttgt aaaagcaaat gatgtatgtat ctcagaagat tgctgaaagg 1050
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caattggatt tcaggttccc tttttgtgc ttcatgcctt acttcttaat 1900
gcctctctaa agccaaa 1917

<210> 205
<211> 392
<212> PRT
<213> *Homo sapiens*

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<400> 205
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Phe Leu Leu Pro Ser Ala Gln Gly Arg Gln Lys Glu Ser Gly Ser
      20          25          30

Lys Trp Lys Val Phe Ile Asp Gln Ile Asn Arg Ser Leu Glu Asn
      35          40          45

Tyr Glu Pro Cys Ser Ser Gln Asn Cys Ser Cys Tyr His Gly Val
      50          55          60

Ile Glu Glu Asp Leu Thr Pro Phe Arg Gly Gly Ile Ser Arg Lys
      65          70          75

Met Met Ala Glu Val Val Arg Arg Lys Leu Gly Thr His Tyr Gln
      80          85          90

Ile Thr Lys Asn Arg Leu Tyr Arg Glu Asn Asp Cys Met Phe Pro

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Ser Arg Cys Ser Gly Val Glu His Phe Ile Leu Glu Val Ile Gly			
110	115	120	
Arg Leu Pro Asp Met Glu Met Val Ile Asn Val Arg Asp Tyr Pro			
125	130	135	
Gln Val Pro Lys Trp Met Glu Pro Ala Ile Pro Val Phe Ser Phe			
140	145	150	
Ser Lys Thr Ser Glu Tyr His Asp Ile Met Tyr Pro Ala Trp Thr			
155	160	165	
Phe Trp Glu Gly Pro Ala Val Trp Pro Ile Tyr Pro Thr Gly			
170	175	180	
Leu Gly Arg Trp Asp Leu Phe Arg Glu Asp Leu Val Arg Ser Ala			
185	190	195	
Ala Gln Trp Pro Trp Lys Lys Asn Ser Thr Ala Tyr Phe Arg			
200	205	210	
Gly Ser Arg Thr Ser Pro Glu Arg Asp Pro Leu Ile Leu Leu Ser			
215	220	225	
Arg Lys Asn Pro Lys Leu Val Asp Ala Glu Tyr Thr Lys Asn Gln			
230	235	240	
Ala Trp Lys Ser Met Lys Asp Thr Leu Gly Lys Pro Ala Ala Lys			
245	250	255	
Asp Val His Leu Val Asp His Cys Lys Tyr Lys Tyr Leu Phe Asn			
260	265	270	
Phe Arg Gly Val Ala Ala Ser Phe Arg Phe Lys His Leu Phe Leu			
275	280	285	
Cys Gly Ser Leu Val Phe His Val Gly Asp Glu Trp Leu Glu Phe			
290	295	300	
Phe Tyr Pro Gln Leu Lys Pro Trp Val His Tyr Ile Pro Val Lys			
305	310	315	
Thr Asp Leu Ser Asn Val Gln Glu Leu Leu Gln Phe Val Lys Ala			
320	325	330	
Asn Asp Asp Val Ala Gln Glu Ile Ala Glu Arg Gly Ser Gln Phe			
335	340	345	
Ile Arg Asn His Leu Gln Met Asp Asp Ile Thr Cys Tyr Trp Glu			
350	355	360	
Asn Leu Leu Ser Glu Tyr Ser Lys Phe Leu Ser Tyr Asn Val Thr			
365	370	375	
Arg Arg Lys Gly Tyr Asp Gln Ile Ile Pro Lys Met Leu Lys Thr			
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Glu Leu			

<210> 206

DRAFT - NOT FOR CITATION

<211> 1425
<212> DNA
<213> Homo sapiens

<400> 206
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ggatgccgc caggatggc tggctgcctgcaggaccgc agcatccttgc 200
ccccctggc atggatctg ggcttcctgc ttctatttgt tggcagcac 250
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aaagtcaaggc tttttctaaa aaaaa 1425

<210> 207
<211> 262
<212> PRT
<213> Homo sapiens

<400> 207
Met Ala Pro Ala Leu Leu Leu Ile Pro Ala Ala Leu Ala Ser Phe
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Ile Leu Ala Phe Gly Thr Gly Val Glu Phe Val Arg Phe Thr Ser
20 25 30
Leu Arg Pro Leu Leu Gly Gly Ile Pro Glu Ser Gly Gly Pro Asp
35 40 45
Ala Arg Gln Gly Trp Leu Ala Ala Leu Gln Asp Arg Ser Ile Leu
50 55 60
Ala Pro Leu Ala Trp Asp Leu Gly Leu Leu Leu Phe Val Gly
65 70 75
Gln His Ser Leu Met Ala Ala Glu Arg Val Lys Ala Trp Thr Ser
80 85 90
Arg Tyr Phe Gly Val Leu Gln Arg Ser Leu Tyr Val Ala Cys Thr
95 100 105
Ala Leu Ala Leu Gln Leu Val Met Arg Tyr Trp Glu Pro Ile Pro
110 115 120
Lys Gly Pro Val Leu Trp Glu Ala Arg Ala Glu Pro Trp Ala Thr
125 130 135
Trp Val Pro Leu Leu Cys Phe Val Leu His Val Ile Ser Trp Leu
140 145 150
Leu Ile Phe Ser Ile Leu Leu Val Phe Asp Tyr Ala Glu Leu Met
155 160 165
Gly Leu Lys Gln Val Tyr Tyr His Val Leu Gly Leu Gly Glu Pro
170 175 180
Leu Ala Leu Lys Ser Pro Arg Ala Leu Arg Leu Phe Ser His Leu
185 190 195
Arg His Pro Val Cys Val Glu Leu Leu Thr Val Leu Trp Val Val
200 205 210
Pro Thr Leu Gly Thr Asp Arg Leu Leu Ala Phe Leu Leu Thr
215 220 225
Leu Tyr Leu Gly Leu Ala His Gly Leu Asp Gln Gln Asp Leu Arg
230 235 240
Tyr Leu Arg Ala Gln Leu Gln Arg Lys Leu His Leu Leu Ser Arg
245 250 255
Pro Gln Asp Gly Glu Ala Glu
260

<210> 208
<211> 2095
<212> DNA

<213> Homo sapiens

<400> 208
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caacaaaaaa cttaagcttt aatttcatct ggaattccac agtttctta 200
gctccctgga cccgggttgac ctgttggctc ttcccgctgg ctgtctatac 250
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caagataaaa aggatagtga atcattctt acatgcaac atttccagt 1950
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tactgtggta atatagagaa gaattaaago aagaaaatct gaaaa 2095

<210> 209

<211> 331

<212> PRT

<213> Homo sapiens

<400> 209

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				20					25					30
Phe	Val	Met	Trp	Tyr	Leu	Ser	Leu	Pro	His	Tyr	Asn	Val	Ile	Glu
				35				40						45
Arg	Val	Asn	Trp	Met	Tyr	Phe	Tyr	Glu	Tyr	Glu	Pro	Ile	Tyr	Arg
				50				55						60
Gln	Asp	Phe	His	Phe	Thr	Leu	Arg	Glu	His	Ser	Asn	Cys	Ser	His
				65				70						75
Gln	Asn	Pro	Phe	Leu	Val	Ile	Leu	Val	Thr	Ser	His	Pro	Ser	Asp
				80				85						90
Val	Lys	Ala	Arg	Gln	Ala	Ile	Arg	Val	Thr	Trp	Gly	Glu	Lys	Lys
				95					100					105
Ser	Trp	Trp	Gly	Tyr	Glu	Val	Leu	Thr	Phe	Phe	Leu	Leu	Gly	Gln
				110					115					120
Glu	Ala	Glu	Lys	Glu	Asp	Lys	Met	Leu	Ala	Leu	Ser	Leu	Glu	Asp
				125					130					135
Glu	His	Leu	Leu	Tyr	Gly	Asp	Ile	Ile	Arg	Gln	Asp	Phe	Leu	Asp
				140					145					150
Thr	Tyr	Asn	Asn	Leu	Thr	Leu	Lys	Thr	Ile	Met	Ala	Phe	Arg	Trp
				155					160					165

Val Thr Glu Phe Cys Pro Asn Ala Lys Tyr Val Met Lys Thr Asp
170 175 180

Thr Asp Val Phe Ile Asn Thr Gly Asn Leu Val Lys Tyr Leu Leu
185 190 195

Asn Leu Asn His Ser Glu Lys Phe Phe Thr Gly Tyr Pro Leu Ile
200 205 210

Asp Asn Tyr Ser Tyr Arg Gly Phe Tyr Gln Lys Thr His Ile Ser
215 220 225

Tyr Gln Glu Tyr Pro Phe Lys Val Phe Pro Pro Tyr Cys Ser Gly
230 235 240

Leu Gly Tyr Ile Met Ser Arg Asp Leu Val Pro Arg Ile Tyr Glu
245 250 255

Met Met Gly His Val Lys Pro Ile Lys Phe Glu Asp Val Tyr Val
260 265 270

Gly Ile Cys Leu Asn Leu Leu Lys Val Asn Ile His Ile Pro Glu
275 280 285

Asp Thr Asn Leu Phe Phe Leu Tyr Arg Ile His Leu Asp Val Cys
290 295 300

Gln Leu Arg Arg Val Ile Ala Ala His Gly Phe Ser Ser Lys Glu
305 310 315

Ile Ile Thr Phe Trp Gln Val Met Leu Arg Asn Thr Thr Cys His
320 325 330

Tyr

<210> 210
<211> 745
<212> DNA
<213> Homo sapiens

<400> 210
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ggacatttcc ttctgtggag acacggtgga gaactaaaca attttttaaa 600
gccactatgg atttagtcat ctgaatatgc tgcagaaa aaatatggc 650
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<210> 211
<211> 185
<212> PRT
<213> Homo sapiens

<400> 211
Met Lys Phe Thr Ile Val Phe Ala Gly Leu Leu Gly Val Phe Leu
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Ala Pro Ala Leu Ala Asn Tyr Asn Ile Asn Val Asn Asp Asp Asn
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Asn Asn Ala Gly Ser Gly Gln Gln Ser Val Ser Val Asn Asn Glu
35 40 45
His Asn Val Ala Asn Val Asp Asn Asn Asn Gly Trp Asp Ser Trp
50 55 60
Asn Ser Ile Trp Asp Tyr Gly Asn Gly Phe Ala Ala Thr Arg Leu
65 70 75
Phe Gln Lys Lys Thr Cys Ile Val His Lys Met Asn Lys Glu Val
80 85 90
Met Pro Ser Ile Gln Ser Leu Asp Ala Leu Val Lys Glu Lys Lys
95 100 105
Leu Gln Gly Lys Pro Gly Gly Pro Pro Lys Gly Leu Met
110 115 120
Tyr Ser Val Asn Pro Asn Lys Val Asp Asp Leu Ser Lys Phe Gly
125 130 135
Lys Asn Ile Ala Asn Met Cys Arg Gly Ile Pro Thr Tyr Met Ala
140 145 150
Glu Glu Met Gln Glu Ala Ser Leu Phe Phe Tyr Ser Gly Thr Cys
155 160 165
Tyr Thr Thr Ser Val Leu Trp Ile Val Asp Ile Ser Phe Cys Gly
170 175 180
Asp Thr Val Glu Asn
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<210> 212
<211> 1706
<212> DNA
<213> Homo sapiens

<400> 212
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atgaaataat taaaaaggc ttgcgtcata tatagaaaa tcgcataatgg 150
tcctagtatt aaatttttat tgcttactga tttttttag ttaagagtt 200
ttatatgcta gaatatgagg atgtaatat aaataagaga agaaaaaaga 250
ataaagtata ttgagtcctcc aattttatgt aagcttcaga agaactggtt 300
tgtttacatg caagcttata gttgaatat tttcaggaa ttacatgaat 350
gacagtcttc gaaccaatgt gtttgtcga tttcaaccag agactatagc 400
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ctcgcccca ttggtttctt cttttggta ctacagaaga ggaaatccag 500
ggaaatctgca tagaaacact taggtttat accagaaaaa agccaaacta 550
tgaattactg gaaaaagaag tagaaaaaaag aaaagtagcc ttacaagaag 600
ccaaattaaa agcaaaggga ttgaatccgg atggaactcc agcccttca 650
accctgggtg gattttctc agcctccaa ccatcatcac caagagaagt 700
aaaagctgaa gagaatcac caatctccat taatgtgaag acagtcaaaa 750
aagaacctga ggatagacaa caggcttca aaagccctta caatggtgta 800
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gtcaagaaca cgatcacgtt ctagatcaca tactccaaga agacactata 900
ataataggcg gagtcgtatc ggaacataca gctcgagatc aagaaggcagg 950
tccccagtc acagtgaag ccctcgaaga catcataatc atggttctcc 1000
tcaccccttaag gccaaggata ccagagatga tttaaaaagt tcaaacagac 1050
atggtcataa aaggaaaaaa ttcgttctc gatctcagag caagtctcg 1100
gatcactcaag atgcagccaa gaaacacagg catgaaagg gacatcatag 1150
ggcagggcgta gaacgatctc gtcctttaa gaggtcccat aaaagcaagc 1200
accatgggtg cagtcgtctca ggacatggca ggcacaggcg ctgactttct 1250
cttcctttaa gcctgcataa gttttgggtt ttgcctatct acagtgtgat 1300
gtatggactc aatcaaaaac attaacgcata aactgattttag gatttgattt 1350
cttggaaaccc tcttaggtctc tagaacactg aggacagttt ctttggaaa 1400
gaactatgtt aatttttttgc cacattaaaa tgccctagca gtatctaatt 1450
aaaaaccatg gtcagggttca attgtactttt attatagttt tgtagttttt 1500
atggctataa gaactggagc gtgaattctg taaaaatgtt tctttttttt 1550
atacagataa aattgcagac actgttctat ttaagtgggtt atttgtttaa 1600
atgatgggtgta atacttttttca aacactgggtt tgctgcata tggaaagatt 1650
tttacaaggaa aataaaatac aatcttggta ttttctaaaa aaaaaaaaaa 1700

aaaaagt 1706

<210> 213

<211> 299

<212> PRT

<213> Homo sapiens

<400> 213

Met	Asn	Asp	Ser	Leu	Arg	Thr	Asn	Val	Phe	Val	Arg	Phe	Gln	Pro
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Glu	Thr	Ile	Ala	Cys	Ala	Cys	Ile	Tyr	Leu	Ala	Ala	Arg	Ala	Leu
20							25					30		

Gln	Ile	Pro	Leu	Pro	Thr	Arg	Pro	His	Trp	Phe	Leu	Leu	Phe	Gly
35								40					45	

Thr	Thr	Glu	Glu	Glu	Ile	Gln	Glu	Ile	Cys	Ile	Glu	Thr	Leu	Arg
50								55				60		

Leu	Tyr	Thr	Arg	Lys	Lys	Pro	Asn	Tyr	Glu	Leu	Leu	Glu	Lys	Glu
65								70				75		

Val	Glu	Lys	Arg	Lys	Val	Ala	Leu	Gln	Glu	Ala	Lys	Leu	Lys	Ala
80								85				90		

Lys	Gly	Leu	Asn	Pro	Asp	Gly	Thr	Pro	Ala	Leu	Ser	Thr	Leu	Gly
95								100				105		

Gly	Phe	Ser	Pro	Ala	Ser	Lys	Pro	Ser	Ser	Pro	Arg	Glu	Val	Lys
110								115				120		

Ala	Glu	Glu	Lys	Ser	Pro	Ile	Ser	Ile	Asn	Val	Lys	Thr	Val	Lys
125								130				135		

Lys	Glu	Pro	Glu	Asp	Arg	Gln	Gln	Ala	Ser	Lys	Ser	Pro	Tyr	Asn
140								145				150		

Gly	Val	Arg	Lys	Asp	Ser	Lys	Arg	Ser	Arg	Asn	Ser	Arg	Ser	Ala
155								160				165		

Ser	Arg	Ser	Arg	Ser	Arg	Thr	Arg	Ser	Arg	Ser	Arg	Ser	His	Thr
170								175				180		

Pro	Arg	Arg	His	Tyr	Asn	Asn	Arg	Arg	Ser	Arg	Ser	Gly	Thr	Tyr
185								190				195		

Ser	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Ser	His	Ser	Glu	Ser	Pro
200								205				210		

Arg	Arg	His	His	Asn	His	Gly	Ser	Pro	His	Leu	Lys	Ala	Lys	His
215								220				225		

Thr	Arg	Asp	Asp	Leu	Lys	Ser	Ser	Asn	Arg	His	Gly	His	Lys	Arg
230								235				240		

Lys	Lys	Ser	Arg	Ser	Arg	Ser	Gln	Ser	Lys	Ser	Arg	Asp	His	Ser
245								250				255		

Asp	Ala	Ala	Lys	Lys	His	Arg	His	Glu	Arg	Gly	His	His	Arg	Asp
260								265				270		

Arg Arg Glu Arg Ser Arg Ser Phe Glu Arg Ser His Lys Ser Lys

275

280

285

His His Gly Gly Ser Arg Ser Gly His Gly Arg Arg His Arg Arg
290 295

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<210> 214
<211> 730
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 72-73, 85, 91, 127, 226, 268, 454, 484, 513, 566, 663
<223> unknown base
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<400> 214
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ggattgtaat atgaaattat taaaaggc ttgcgtcata tatagaaaa 200
tcgcataatgg tcctagtatt aaatnttat tgcttactga ttttttgag 250
ttaagagttt ttatatgnta gaatatgagg atgtgaatat aaataagaga 300
agaaaaaaga ataaagtata ttgagtctcc aattttatgt aagcttcaga 350
agaactggtt tgtttacatg caagcttata gttgaaatat ttttcaggaa 400
ttacatgaat gacagtcttc gaaccatgt gtttggcga tttcaaccag 450
agantatacg atgtgttgc atctacacctg cagnatagc accttcaggat 500
ccgttgccaa ctngtccccca ttggtttctt ctttttggta ctacagaaga 550
ggaaatcccg gaaatntgc tagaaacact taggctttat accagaaaaaa 600
agccaaacta tgaattactg gaaaaagaag tagaaaaaaag aaaagttagcc 650
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agccctttca accctgggtt gattttctcc 730

<210> 215
<211> 1807
<212> DNA
<213> *Homo sapiens*

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ctctgtaaacg gcagtttgtt ccgataacaag caccctgtcg aggaggagct 200
tcggggccctg gggggaaagg cgaggccccag aggcaggaaaa gagcggtggg 250
ccaatggccct tagtggggaa aqccactgt ctgtcccccg agatggcccg 300
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TOP SECRET 6650

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cttcttcctg gaggaccgt ggtttgtga ctgtgtgt tactcggcg 400
gcgtgtacct cttcacagag gcctactact acatgctggg accagccaag 450
gagactaaca ttgtgtgtt ctggcgtcg ctcacggta ccttctccat 500
caagatgttc ctgacagtga cacggctgtc cttcagcgcc gaggagggg 550
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tggtctggcc agcatgaccc agaaacttaga gccacttctg aagaagcagg 700
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gcagtggtgg gctctgtgtc ggggccttc ctcaccccttc cagggctgcg 800
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<210> 216

<211> 479
<212> PRT
<213> Homo sapiens

<400> 216
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35 40 45
Glu Glu Leu Arg Ala Leu Ala Gly Lys Pro Arg Pro Arg Gly Arg
50 55 60
Lys Glu Arg Trp Ala Asn Gly Leu Ser Glu Glu Lys Pro Leu Ser
65 70 75
Val Pro Arg Asp Ala Pro Phe Gln Leu Glu Thr Cys Pro Leu Thr
80 85 90
Thr Val Asp Ala Leu Val Leu Arg Phe Phe Leu Glu Tyr Gln Trp
95 100 105
Phe Val Asp Phe Ala Val Tyr Ser Gly Gly Val Tyr Leu Phe Thr
110 115 120
Glu Ala Tyr Tyr Tyr Met Leu Gly Pro Ala Lys Glu Thr Asn Ile
125 130 135
Ala Val Phe Trp Cys Leu Leu Thr Val Thr Phe Ser Ile Lys Met
140 145 150
Phe Leu Thr Val Thr Arg Leu Tyr Phe Ser Ala Glu Glu Gly
155 160 165
Glu Arg Ser Val Cys Leu Thr Phe Ala Phe Leu Phe Leu Leu
170 175 180
Ala Met Leu Val Gln Val Val Arg Glu Glu Thr Leu Glu Leu Gly
185 190 195
Leu Glu Pro Gly Leu Ala Ser Met Thr Gln Asn Leu Glu Pro Leu
200 205 210
Leu Lys Lys Gln Gly Trp Asp Trp Ala Leu Pro Val Ala Lys Leu
215 220 225
Ala Ile Arg Val Gly Leu Ala Val Val Gly Ser Val Leu Gly Ala
230 235 240
Phe Leu Thr Phe Pro Gly Leu Arg Leu Ala Gln Thr His Arg Asp
245 250 255
Ala Leu Thr Met Ser Glu Asp Arg Pro Met Leu Gln Phe Leu Leu
260 265 270
His Thr Ser Phe Leu Ser Pro Leu Phe Ile Leu Trp Leu Trp Thr
275 280 285
Lys Pro Ile Ala Arg Asp Phe Leu His Gln Pro Pro Phe Gly Glu

290	295	300
Thr Arg Phe Ser Leu Leu Ser Asp Ser Ala	Phe Asp Ser Gly Arg	
305 310	315	
Leu Trp Leu Leu Val Val Leu Cys Leu	Leu Arg Leu Ala Val Thr	
320	325	330
Arg Pro His Leu Gln Ala Tyr Leu Cys	Leu Ala Lys Ala Arg Val	
335	340	345
Glu Gln Leu Arg Arg Glu Ala Gly Arg Ile	Glu Ala Arg Glu Ile	
350	355	360
Gln Gln Arg Val Val Arg Val Tyr Cys	Tyr Val Thr Val Val Ser	
365	370	375
Leu Gln Tyr Leu Thr Pro Leu Ile Leu	Thr Leu Asn Cys Thr Leu	
380	385	390
Leu Leu Lys Thr Leu Gly Gly Tyr Ser Trp	Gly Leu Gly Pro Ala	
395	400	405
Pro Leu Leu Ser Pro Asp Pro Ser Ser Ala	Ser Ala Ala Pro Ile	
410	415	420
Gly Ser Gly Glu Asp Glu Val Gln Gln	Thr Ala Ala Arg Ile Ala	
425	430	435
Gly Ala Leu Gly Gly Leu Leu Thr Pro	Leu Phe Leu Arg Gly Val	
440	445	450
Leu Ala Tyr Leu Ile Trp Trp Thr Ala Ala	Cys Gln Leu Leu Ala	
455	460	465
Ser Leu Phe Gly Leu Tyr Phe His Gln His	Leu Ala Gly Ser	
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<210> 217
<211> 574
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 5, 146
<223> unknown base

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gctggctgtctgtaaacggc agtttggccataacaagca cccgtnttga 150
ggaggagctt cggggccctgg cggggaaagcc gaggcccaga ggcaggaaag 200
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actcggggcg cggttacctc ttccacagagg cctactacta catgctggga 400
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<210> 218
<211> 2571
<212> DNA
<213> Homo sapiens

<400> 218
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ggctgggtt ggccttgc gctgacagaa ggtggccagg gagaatgcag 200
cacactgctc ggagaatgaa ggogcttcg ttgctggct tgcctggct 250
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cagaactctg taaagggtgcc tcccactacg gcctgaccaa agatagggaa 350
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agaatgaccc tgtgttagcc atcaatggac atgatcttcg atatggcagc 1250
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caccagcata caatgtggaa agaatttagat gtggtgatat tctttttgt 2000
gtcaatggta gaagtacatc aggaatgata catgcttgc tggcaagact 2050
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tgtataccctt actgaattca agctgattta aattttttat ttggttatgt 2450
ctgaagtctg ccaagggtac attatggcca tttttttat acagctaaaa 2500
tattttttttaa aatgcatttc tgagaaacgt tgctttcato aaacaagaat 2550
aaatattttt cagaaggtaa a 2571

<210> 219
<211> 632
<212> PRT
<213> Homo sapiens

<400> 219
Met Lys Ala Leu Leu Leu Val Leu Pro Trp Leu Ser Pro Ala

1 5 10 15

Asn	Tyr	Ile	Asp	Asn	Val	Gly	Asn	Leu	His	Phe	Leu	Tyr	Ser	Glu
				20				25					30	

Leu	Cys	Lys	Gly	Ala	Ser	His	Tyr	Gly	Leu	Thr	Lys	Asp	Arg	Lys
				35				40					45	

Arg	Arg	Ser	Gln	Asp	Gly	Cys	Pro	Asp	Gly	Cys	Ala	Ser	Leu	Thr
				50				55					60	

Ala	Thr	Ala	Pro	Ser	Pro	Glu	Val	Ser	Ala	Ala	Ala	Thr	Ile	Ser
				65				70					75	

Leu	Met	Thr	Asp	Glu	Pro	Gly	Leu	Asp	Asn	Pro	Ala	Tyr	Val	Ser
				80				85					90	

Ser	Ala	Glu	Asp	Gly	Gln	Pro	Ala	Ile	Ser	Pro	Val	Asp	Ser	Gly
				95					100				105	

Arg	Ser	Asn	Arg	Thr	Arg	Ala	Arg	Pro	Phe	Glu	Arg	Ser	Thr	Ile
				110				115					120	

Arg	Ser	Arg	Ser	Phe	Lys	Lys	Ile	Asn	Arg	Ala	Leu	Ser	Val	Leu
				125				130					135	

Arg	Arg	Thr	Lys	Ser	Gly	Ser	Ala	Val	Ala	Asn	His	Ala	Asp	Gln
				140				145					150	

Gly	Arg	Glu	Asn	Ser	Glu	Asn	Thr	Thr	Ala	Pro	Glu	Val	Phe	Pro
				155				160					165	

Arg	Leu	Tyr	His	Leu	Ile	Pro	Asp	Gly	Glu	Ile	Thr	Ser	Ile	Lys
				170				175					180	

Ile	Asn	Arg	Val	Asp	Pro	Ser	Glu	Ser	Leu	Ser	Ile	Arg	Leu	Val
				185				190					195	

Gly	Gly	Ser	Glu	Thr	Pro	Leu	Val	His	Ile	Ile	Ile	Gln	His	Ile
				200				205					210	

Tyr	Arg	Asp	Gly	Val	Ile	Ala	Arg	Asp	Gly	Arg	Leu	Leu	Pro	Gly
				215				220					225	

Asp	Ile	Ile	Leu	Lys	Val	Asn	Gly	Met	Asp	Ile	Ser	Asn	Val	Pro
				230				235					240	

His	Asn	Tyr	Ala	Val	Arg	Leu	Leu	Arg	Gln	Pro	Cys	Gln	Val	Leu
				245				250					255	

Trp	Leu	Thr	Val	Met	Arg	Glu	Gln	Lys	Phe	Arg	Ser	Arg	Asn	Asn
				260				265					270	

Gly	Gln	Ala	Pro	Asp	Ala	Tyr	Arg	Pro	Arg	Asp	Asp	Ser	Phe	His
				275				280					285	

Val	Ile	Leu	Asn	Lys	Ser	Ser	Pro	Glu	Glu	Gln	Leu	Gly	Ile	Lys
				290				295					300	

Leu	Val	Arg	Lys	Val	Asp	Glu	Pro	Gly	Val	Phe	Ile	Phe	Asn	Val
				305				310					315	

Leu Asp Gly Gly Val Ala Tyr Arg His Gly Gln Leu Glu Glu Asn

320	325	330
Asp Arg Val Leu Ala Ile Asn Gly His Asp Leu Arg Tyr Gly Ser 335	340	345
Pro Glu Ser Ala Ala His Leu Ile Gln Ala Ser Glu Arg Arg Val 350	355	360
His Leu Val Val Ser Arg Gln Val Arg Gln Arg Ser Pro Asp Ile 365	370	375
Phe Gln Glu Ala Gly Trp Asn Ser Asn Gly Ser Trp Ser Pro Gly 380	385	390
Pro Gly Glu Arg Ser Asn Thr Pro Lys Pro Leu His Pro Thr Ile 395	400	405
Thr Cys His Glu Lys Val Val Asn Ile Gln Lys Asp Pro Gly Glu 410	415	420
Ser Leu Gly Met Thr Val Ala Gly Gly Ala Ser His Arg Glu Trp 425	430	435
Asp Leu Pro Ile Tyr Val Ile Ser Val Glu Pro Gly Gly Val Ile 440	445	450
Ser Arg Asp Gly Arg Ile Lys Thr Gly Asp Ile Leu Leu Asn Val 455	460	465
Asp Gly Val Glu Leu Thr Glu Val Ser Arg Ser Glu Ala Val Ala 470	475	480
Leu Leu Lys Arg Thr Ser Ser Ser Ile Val Leu Lys Ala Leu Glu 485	490	495
Val Lys Glu Tyr Glu Pro Gln Glu Asp Cys Ser Ser Pro Ala Ala 500	505	510
Leu Asp Ser Asn His Asn Met Ala Pro Pro Ser Asp Trp Ser Pro 515	520	525
Ser Trp Val Met Trp Leu Glu Leu Pro Arg Cys Leu Tyr Asn Cys 530	535	540
Lys Asp Ile Val Leu Arg Arg Asn Thr Ala Gly Ser Leu Gly Phe 545	550	555
Cys Ile Val Gly Gly Tyr Glu Glu Tyr Asn Gly Asn Lys Pro Phe 560	565	570
Phe Ile Lys Ser Ile Val Glu Gly Thr Pro Ala Tyr Asn Asp Gly 575	580	585
Arg Ile Arg Cys Gly Asp Ile Leu Leu Ala Val Asn Gly Arg Ser 590	595	600
Thr Ser Gly Met Ile His Ala Cys Leu Ala Arg Leu Leu Lys Glu 605	610	615
Leu Lys Gly Arg Ile Thr Leu Thr Ile Val Ser Trp Pro Gly Thr 620	625	630
Phe Leu		

<210> 220
<211> 773
<212> DNA
<213> Homo sapiens

<400> 220
ccaaagtat catttggaaa agagatatcc acatcttcaa gcccataaa 50
aggatagaag ctgcacaggg cagcttact tactccagca cttcccttc 100
ccaggcaaat ggtgctgacc atctttggga tacaatctca tggatacgag 150
gttttaaca tcatcagccc aagcaacaat ggtggcaatg ttcaggagac 200
agtgacaatt gataatgaaa aaaataccgc catcgtaac atccatgcag 250
gatcatgctc ttctaccaca attttgact ataaacatgg ctacattgca 300
tccagggtgc tctcccaag agcctgctt atcctgaaga tggaccatca 350
gaacatccct cctctgaaca atctccaatg gtacatctat gagaacagg 400
ctctggacaa catgttctcc aacaaataca cctgggtcaa gtacaaccct 450
ctggagtctc tgatcaaaga cgtggattgg ttccctgctt ggtcacccat 500
tgagaaactc tgcaaacata tccctttgta taaggggaa gtggttgaaa 550
acacacataa tgtcggtgct ggaggctgtg caaaggctgg gctctggc 600
atcttggaa ttcaatctg tgcagacatt catgtttagg atgattagcc 650
cttttgtttt atctttcaa agaaatacat cttgttta cactcaaaag 700
tcaaattaaa ttctttccca atgccccaaac taattttag attcagtcag 750
aaaatataaa tgctgttattt ata 773

<210> 221
<211> 184
<212> PRT
<213> Homo sapiens

<400> 221
Met Lys Ile Leu Val Ala Phe Leu Val Val Leu Thr Ile Phe Gly
1 5 10 15
Ile Gln Ser His Gly Tyr Glu Val Phe Asn Ile Ile Ser Pro Ser
20 25 30
Asn Asn Gly Gly Asn Val Gln Glu Thr Val Thr Ile Asp Asn Glu
35 40 45
Lys Asn Thr Ala Ile Val Asn Ile His Ala Gly Ser Cys Ser Ser
50 55 60
Thr Thr Ile Phe Asp Tyr Lys His Gly Tyr Ile Ala Ser Arg Val
65 70 75
Leu Ser Arg Arg Ala Cys Phe Ile Leu Lys Met Asp His Gln Asn
80 85 90

Ile Pro Pro Leu Asn Asn Leu Gln Trp Tyr Ile Tyr Glu Lys Gln
95 100 105

Ala Leu Asp Asn Met Phe Ser Asn Lys Tyr Thr Trp Val Lys Tyr
110 115 120

Asn Pro Leu Glu Ser Leu Ile Lys Asp Val Asp Trp Phe Leu Leu
125 130 135

Gly Ser Pro Ile Glu Lys Leu Cys Lys His Ile Pro Leu Tyr Lys
140 145 150

Gly Glu Val Val Glu Asn Thr His Asn Val Gly Ala Gly Gly Cys
155 160 165

Ala Lys Ala Gly Leu Leu Gly Ile Leu Gly Ile Ser Ile Cys Ala
170 175 180

Asp Ile His Val

<210> 222

<211> 992

<212> DNA

<213> Homo sapiens

<400> 222
ggcacgagcc aggaacttagg aggttctcac tgccc gagca gaggccctac 50
acccaccgag gcatgggct ccctgggctg ttctgcttg cctgtctggc 100
tgccagcagc ttctccaagg cacgggagga agaaattacc cctgtgtct 150
ccattgccta caaagtccctg gaagtttcc ccaaaggccg ctgggtgctc 200
ataaacctgct gtgcacccca gccaccaccc cccatcacct attccctctg 250
tggaaccaag aacatcaagg tggcaagaa ggtggtaag acccacgagc 300
cgccctccctt caacctcaac gtcacactca agtccagtc agacctgctc 350
acctaacttct gccccctc tcacactca ggtgcccattg tggacagtgc 400
caggctacag atgcactggg agctgtggtc caagccagtg tctgagctgc 450
gggcaactt cactctcgac gacagagggg caggccccag ggtggagatg 500
atctgcaggc cgtcctcggg cagccccacct atcaccaaca gcctgatcg 550
gaaggatggg cagggtccacc tgcagcagag accatgccac aggccatctg 600
ccaaacttctc cttccctcgcc agccagacat cgactgtt ctgggtccag 650
gctgcaaaca acgccaatgt ccagcacagc gcctcacag tggcccccc 700
aggtgttgcac cagaagatgg aggactggca ggtccccctg gagagcccc 750
tccttgcctt gccgtctac aggacaccg gccgtctgag tgaagaggag 800
tttgggggtt tcagatagg gaatggggag gtcagaggac gcaaagcagc 850
agccatgttag aatgaaccgt ccagagagcc aagcacggca gaggactgca 900

ggccatcago gtgcactgtt cgtatttggaa gttcatgcaa aatgagtgtg 950
 ttttagctgc tcttgccaca aaaaaaaaaa aaaaaaaaaa aa 992
 <210> 223
 <211> 265
 <212> PRT
 <213> Homo sapiens
 <400> 223
 Met Gly Leu Pro Gly Leu Phe Cys Leu Ala Val Leu Ala Ala Ser
 1 5 10 15
 Ser Phe Ser Lys Ala Arg Glu Glu Glu Ile Thr Pro Val Val Ser
 20 25 30
 Ile Ala Tyr Lys Val Leu Glu Val Phe Pro Lys Gly Arg Trp Val
 35 40 45
 Leu Ile Thr Cys Cys Ala Pro Gln Pro Pro Pro Pro Ile Thr Tyr
 50 55 60
 Ser Leu Cys Gly Thr Lys Asn Ile Lys Val Ala Lys Lys Val Val
 65 70 75
 Lys Thr His Glu Pro Ala Ser Phe Asn Leu Asn Val Thr Leu Lys
 80 85 90
 Ser Ser Pro Asp Leu Leu Thr Tyr Phe Cys Arg Ala Ser Ser Thr
 95 100 105
 Ser Gly Ala His Val Asp Ser Ala Arg Leu Gln Met His Trp Glu
 110 115 120
 Leu Trp Ser Lys Pro Val Ser Glu Leu Arg Ala Asn Phe Thr Leu
 125 130 135
 Gln Asp Arg Gly Ala Gly Pro Arg Val Glu Met Ile Cys Gln Ala
 140 145 150
 Ser Ser Gly Ser Pro Pro Ile Thr Asn Ser Leu Ile Gly Lys Asp
 155 160 165
 Gly Gln Val His Leu Gln Gln Arg Pro Cys His Arg Gln Pro Ala
 170 175 180
 Asn Phe Ser Phe Leu Pro Ser Gln Thr Ser Asp Trp Phe Trp Cys
 185 190 195
 Gln Ala Ala Asn Asn Ala Asn Val Gln His Ser Ala Leu Thr Val
 200 205 210
 Val Pro Pro Gly Gly Asp Gln Lys Met Glu Asp Trp Gln Gly Pro
 215 220 225
 Leu Glu Ser Pro Ile Leu Ala Leu Pro Leu Tyr Arg Ser Thr Arg
 230 235 240
 Arg Leu Ser Glu Glu Glu Phe Gly Gly Phe Arg Ile Gly Asn Gly
 245 250 255
 Glu Val Arg Gly Arg Lys Ala Ala Ala Met
 260 265

<210> 224
<211> 1297
<212> DNA
<213> Homo sapiens

<400> 224
ggtccttaat ggcagcagcc gcccgttacca agatccttct gtgcctccccg 50
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ctctctttgc tatgacatcc cccgtcatccc taagttcaga cctggaccac 150
ggtggtgtgc gggtcaaggc cagggtggatg aaaagacttt tcttcactat 200
gactgtggca acaagacagt cacacactgtc agtcccctgg ggaagaaaact 250
aaatgtcaca acggccgttga aagcacagaa cccagttactg agagaggtgg 300
tggacatact tacagagcaa ctgcgtgaca tttagtggaa gaattacaca 350
cccaagggAAC ccctcacccgt gcaggcaagg atgtcttgcg agcagaaaAGC 400
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gccagaaaaAGA tgaaagaaaa gtggggaaat gacaagggttgc tggccatgtc 550
cttccattac ttctcaatgg gagactgtat aggatggctt gaggacttct 600
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tgatattttaa ataaagaggctt atttccca aaaaaaaaaaaaaaaa 1297

<210> 225
<211> 246
<212> PRT
<213> Homo sapiens

<400> 225
 Met Ala Ala Ala Ala Ala Thr Lys Ile Leu Leu Cys Leu Pro Leu
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 Leu Leu Leu Ser Gly Trp Ser Arg Ala Gly Arg Ala Asp Pro
 20 25 30
 His Ser Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro
 35 40 45
 Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
 50 55 60
 Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser
 65 70 75
 Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln
 80 85 90
 Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu
 95 100 105
 Arg Asp Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr
 110 115 120
 Leu Gln Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser
 125 130 135
 Ser Gly Ser Trp Gln Phe Ser Phe Asp Gly Gln Ile Phe Leu Leu
 140 145 150
 Phe Asp Ser Glu Lys Arg Met Trp Thr Thr Val His Pro Gly Ala
 155 160 165
 Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys Val Val Ala Met
 170 175 180
 Ser Phe His Tyr Phe Ser Met Gly Asp Cys Ile Gly Trp Leu Glu
 185 190 195
 Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser Ala Gly
 200 205 210
 Ala Pro Leu Ala Met Ser Ser Gly Thr Thr Gln Leu Arg Ala Thr
 215 220 225
 Ala Thr Thr Leu Ile Leu Cys Cys Leu Leu Ile Ile Leu Pro Cys
 230 235 240
 Phe Ile Leu Pro Gly Ile
 245

<210> 226
 <211> 735
 <212> DNA
 <213> Homo sapiens

<400> 226
 gggaaaggcca tttcgaaaac ccatctatac aaactatata ttttcatttc 50
 tgctgctagc tgccttgggc ctcacaattt tcattctgtt ttctgacttt 100
 caagttatat accgtggaat ggagttgatc ccaaccataa catcgtggag 150

ggtttaatt ttgggttag ccctcacca attctggtgt ggcttcttt 200
gcagaggatt ccaccccaa aatcatgaaat tctggcttt gatcaaaaaga 250
gaatttggat tctactctaa aagtcaataat aggacttggc aaaagaagct 300
agcagaagac tcaacccggc ctcccataaa caggacagat tattcagggt 350
atggcaaaaa ttggattctac atcaacggag gctatgaaag ccatgaacag 400
attccaaaaa gaaaactcaa attggggcag caaccacag aacagcattt 450
ctggccagg ctgtaatcg aattgtcg tcgtatgctc aacagcattt 500
ctttttccc caaaattaac acattgtgaa gaagtgtatga tactttcccc 550
ttacccccc tctctccatt caagcattca aagtatattt tcaatgaatt 600
aaacccgtca gcaagggacc ttagataggc ttattctgac tgtatgctt 650
accaatgaga gaaaaaaatg catttcgtt atcatccctt tcaataaaact 700
gtattcatt tgaaaaaaaaaaaaaaaaaaaa 735

<210> 227

<211> 115

<212> PRT

<213> Homo sapiens

<400> 227

Met	Glu	Leu	Ile	Pro	Thr	Ile	Thr	Ser	Trp	Arg	Val	Leu	Ile	Leu
1									10					15

Val	Val	Ala	Leu	Thr	Gln	Phe	Trp	Cys	Gly	Phe	Leu	Cys	Arg	Gly
						20			25					30

Phe	His	Leu	Gln	Asn	His	Glu	Leu	Trp	Leu	Ile	Lys	Arg	Glu
						35			40				45

Phe	Gly	Phe	Tyr	Ser	Lys	Ser	Gln	Tyr	Arg	Thr	Trp	Gln	Lys	Lys
						50			55				60	

Leu	Ala	Glu	Asp	Ser	Thr	Trp	Pro	Pro	Ile	Asn	Arg	Thr	Asp	Tyr
									65				70	75

Ser	Gly	Asp	Gly	Lys	Asn	Gly	Phe	Tyr	Ile	Asn	Gly	Tyr	Glu
						80				85			90

Ser	His	Glu	Gln	Ile	Pro	Lys	Arg	Lys	Leu	Lys	Leu	Gly	Gln
						95			100				105

Pro	Thr	Glu	Gln	His	Phe	Trp	Ala	Arg	Leu
									110
									115

<210> 228

<211> 2185

<212> DNA

<213> Homo sapiens

<400> 228

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cacaccatga agctttgtg gcaggttaact gtgcaccacc acacccggaa 100

tgccatcctg ctcccgttcg tctacacctac ggccgcaagtg tggattctgt 150
gtgcagccat cgctgctgcc gcctcagccg ggccccagaa ctgccccctcc 200
gtttgctcggt gcagtaacca gttcagcaag gtgggtgtca cgcgcgggg 250
cctctccgag gtcccgagg gtattccctc gaacacccgg tacctaacc 300
tcatggagaa caacatccag atgatccagg ccgacaccc ttccgcaccc 350
caccacctgg aggtcctgc gttggcagg aactccatcc ggcagattga 400
ggtggggcc ttcaacggcc tggccagcc caacaccctg gagctgttcg 450
acaactgctc gacagtccatc cctagegggg cctttaataa cctgtccaaag 500
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ccaaggatct ctgtccctcaa cgacggcacc ttgaactttt cccacgtgtt 1300
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actccaacgc ctggccctac ctcaatgtt gacccggctga gcttaacacc 1400
tccaaactaca gcttcccttac cacagtaaca gtggagacca cggagatctc 1450
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gttaccagcc ggcataacc acctcttacca cggtgctcat tcagactacc 1550
cgtgtggcca agcagggtggc agtacccgcg acagacacca ctgacaagat 1600
gcagaccaggc ctggatgaag tcatgaagac caccacccatc atcattggct 1650
gctttgtggc agtgactcttctt ctagctggccg ccatgttgat tggccat 1700

aaacttcgta agcggcacca gcagcggagt acagtcacag ccgccccgac 1750
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cagcaacagc agctccgtcc ggtgtatcg gtgagggggc agtagtgctg 1850
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ccactatctc tgaaccttat ataattcaga cccataccaa ggacaaggta 2000
cagggaaactc aaatatgact cccctcccc aaaaaactta taaaatgcaa 2050
tagaatgcac acaaagacag caactttgt acagagtgg gagagactt 2100
ttcttgata tgcttata ttaagtctat gggctggta aaaaaaacag 2150
attatattaa aatttaaga caaaaagtca aaaca 2185

<210> 229
<211> 653
<212> PRT
<213> Homo sapiens

<400> 229
Met Lys Leu Leu Trp Gln Val Thr Val His His His Thr Trp Asn
1 5 10 15
Ala Ile Leu Leu Pro Phe Val Tyr Leu Thr Ala Gln Val Trp Ile
20 25 30
Leu Cys Ala Ala Ile Ala Ala Ala Ser Ala Gly Pro Gln Asn
35 40 45
Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val Val
50 55 60
Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser
65 70 75
Asn Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile Gln Met Ile
80 85 90
Gln Ala Asp Thr Phe Arg His His Leu Glu Val Leu Gln
95 100 105
Leu Gly Arg Asn Ser Ile Arg Gln Ile Glu Val Gly Ala Phe Asn
110 115 120
Gly Leu Ala Ser Leu Asn Thr Leu Glu Leu Phe Asp Asn Trp Leu
125 130 135
Thr Val Ile Pro Ser Gly Ala Phe Glu Tyr Leu Ser Lys Leu Arg
140 145 150
Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser Tyr
155 160 165
Ala Phe Asn Arg Val Pro Ser Leu Met Arg Leu Asp Leu Gly Glu
170 175 180
Leu Lys Lys Leu Glu Tyr Ile Ser Glu Gly Ala Phe Glu Gly Leu

185	190	195
Phe Asn Leu Lys Tyr	Leu Asn Leu Gly	Met Cys Asn Ile Lys Asp
200	205	210
Met Pro Asn Leu Thr	Pro Leu Val Gly	Leu Glu Glu Leu Glu Met
215	220	225
Ser Gly Asn His Phe	Pro Glu Ile Arg	Pro Gly Ser Phe His Gly
230	235	240
Leu Ser Ser Leu Lys	Lys Leu Trp Val	Met Asn Ser Gln Val Ser
245	250	255
Leu Ile Glu Arg Asn Ala	Phe Asp Gly	Leu Ala Ser Leu Val Glu
260	265	270
Leu Asn Leu Ala His	Asn Asn Leu Ser	Ser Leu Pro His Asp Leu
275	280	285
Phe Thr Pro Leu Arg	Tyr Leu Val Glu	Leu His Leu His His Asn
290	295	300
Pro Trp Asn Cys Asp	Cys Asp Ile Leu	Trp Leu Ala Trp Trp Leu
305	310	315
Arg Glu Tyr Ile Pro	Thr Asn Ser Thr	Cys Cys Gly Arg Cys His
320	325	330
Ala Pro Met His Met	Arg Gly Arg Tyr	Leu Val Glu Val Asp Gln
335	340	345
Ala Ser Phe Gln Cys	Ser Ala Pro Phe	Ile Met Asp Ala Pro Arg
350	355	360
Asp Leu Asn Ile Ser	Glu Gly Arg Met	Ala Glu Leu Lys Cys Arg
365	370	375
Thr Pro Pro Met Ser	Ser Val Lys Trp	Leu Leu Pro Asn Gly Thr
380	385	390
Val Leu Ser His Ala	Ser Arg His Pro Arg	Ile Ser Val Leu Asn
395	400	405
Asp Gly Thr Leu Asn	Phe Ser His Val	Leu Leu Ser Asp Thr Gly
410	415	420
Val Tyr Thr Cys Met	Val Thr Asn Val	Ala Gly Asn Ser Asn Ala
425	430	435
Ser Ala Tyr Leu Asn	Val Ser Thr Ala	Glu Leu Asn Thr Ser Asn
440	445	450
Tyr Ser Phe Phe	Thr Thr Val	Glu Thr Thr Glu Ile Ser
455	460	465
Pro Glu Asp Thr	Thr Arg Lys Tyr	Lys Pro Val Pro Thr Thr Ser
470	475	480
Thr Gly Tyr Gln Pro	Ala Tyr Thr	Ser Thr Thr Val Leu Ile
485	490	495
Gln Thr Thr Arg Val	Pro Lys Gln Val	Ala Val Pro Ala Thr Asp

500	505	510
Thr Thr Asp Lys Met Gln Thr Ser Leu Asp Glu Val Val Met Lys Thr		
515	520	525
Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Val Thr Leu Leu Ala		
530	535	540
Ala Ala Met Leu Ile Val Phe Tyr Lys Leu Arg Lys Arg His Gln		
545	550	555
Gln Arg Ser Thr Val Thr Ala Ala Arg Thr Val Glu Ile Ile Gln		
560	565	570
Val Asp Glu Asp Ile Pro Ala Ala Thr Ser Ala Ala Ala Thr Ala		
575	580	585
Ala Pro Ser Gly Val Ser Gly Glu Gly Ala Val Val Leu Pro Thr		
590	595	600
Ile His Asp His Ile Asn Tyr Asn Thr Tyr Lys Pro Ala His Gly		
605	610	615
Ala His Trp Thr Glu Asn Ser Leu Gly Asn Ser Leu His Pro Thr		
620	625	630
Val Thr Thr Ile Ser Glu Pro Tyr Ile Ile Gln Thr His Thr Lys		
635	640	645
Asp Lys Val Gln Glu Thr Gln Ile		
650		

<210> 230
<211> 2846
<212> DNA
<213> Homo sapiens

<400> 230
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tacacagtca ttaatgaagc ctgccttgc gcagagtggaa atatcatgtg 150
tcgggagtgc tgtgaatatg atcagattga gtgcgtctgc cccggaaaga 200
ggaaagtgcgt gggttataacc atcccttgct gcaggaatga ggagaatgag 250
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aaggtatccc ctaaatgctc actgtgaatg gaccattcat gctaaacctg 500
gttttgtcat ccaactaaga tttgtcatgt tgagtctggaa gtttgactac 550
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agtgtgcctg cttggcggc tatactgggc agcgctgtga aaatccctt 850
gaagaaagaa actgctcaga ccctggggc ccagtcaatg ggtaccagaa 900
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gcttctgaac tacaaaaaaaaaaaaaaa 2750
aaaaaaaaaaaaaaa 2800
aaaaaaaaaaaaaaa 2846

<210> 231

<211> 720

<212> PRT

<213> Homo sapiens

<400> 231
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Glu Ala Cys Pro Gly Ala Glu Trp Asn Ile Met Cys Arg Glu Cys
35 40 45
Cys Glu Tyr Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu
50 55 60
Val Val Gly Tyr Thr Ile Pro Cys Cys Arg Asn Glu Glu Asn Glu
65 70 75
Cys Asp Ser Cys Leu Ile His Pro Gly Cys Thr Ile Phe Glu Asn
80 85 90
Cys Lys Ser Cys Arg Asn Gly Ser Trp Gly Gly Thr Leu Asp Asp
95 100 105
Phe Tyr Val Lys Gly Phe Tyr Cys Ala Glu Cys Arg Ala Gly Trp
110 115 120
Tyr Gly Gly Asp Cys Met Arg Cys Gly Gln Val Leu Arg Ala Pro
125 130 135
Lys Gly Gln Ile Leu Leu Glu Ser Tyr Pro Leu Asn Ala His Cys
140 145 150
Glu Trp Thr Ile His Ala Lys Pro Gly Phe Val Ile Gln Leu Arg
155 160 165

Phe Val Met Leu Ser Leu Glu Phe Asp Tyr Met Cys Gln Tyr Asp
 170 175 180
 Tyr Val Glu Val Arg Asp Gly Asp Asn Arg Asp Gly Gln Ile Ile
 185 190 195
 Lys Arg Val Cys Gly Asn Glu Arg Pro Ala Pro Ile Gln Ser Ile
 200 205 210
 Gly Ser Ser Leu His Val Leu Phe His Ser Asp Gly Ser Lys Asn
 215 220 225
 Phe Asp Gly Phe His Ala Ile Tyr Glu Glu Ile Thr Ala Cys Ser
 230 235 240
 Ser Ser Pro Cys Phe His Asp Gly Thr Cys Val Leu Asp Lys Ala
 245 250 255
 Gly Ser Tyr Lys Cys Ala Cys Leu Ala Gly Tyr Thr Gly Gln Arg
 260 265 270
 Cys Glu Asn Leu Leu Glu Glu Arg Asn Cys Ser Asp Pro Gly Gly
 275 280 285
 Pro Val Asn Gly Tyr Gln Lys Ile Thr Gly Gly Pro Gly Leu Ile
 290 295 300
 Asn Gly Arg His Ala Lys Ile Gly Thr Val Val Ser Phe Phe Cys
 305 310 315
 Asn Asn Ser Tyr Val Leu Ser Gly Asn Glu Lys Arg Thr Cys Gln
 320 325 330
 Gln Asn Gly Glu Trp Ser Gly Lys Gln Pro Ile Cys Ile Lys Ala
 335 340 345
 Cys Arg Glu Pro Lys Ile Ser Asp Leu Val Arg Arg Arg Val Leu
 350 355 360
 Pro Met Gln Val Gln Ser Arg Glu Thr Pro Leu His Gln Leu Tyr
 365 370 375
 Ser Ala Ala Phe Ser Lys Gln Lys Leu Gln Ser Ala Pro Thr Lys
 380 385 390
 Lys Pro Ala Leu Pro Phe Gly Asp Leu Pro Met Gly Tyr Gln His
 395 400 405
 Leu His Thr Gln Leu Gln Tyr Glu Cys Ile Ser Pro Phe Tyr Arg
 410 415 420
 Arg Leu Gly Ser Ser Arg Arg Thr Cys Leu Arg Thr Gly Lys Trp
 425 430 435
 Ser Gly Arg Ala Pro Ser Cys Ile Pro Ile Cys Gly Lys Ile Glu
 440 445 450
 Asn Ile Thr Ala Pro Lys Thr Gln Gly Leu Arg Trp Pro Trp Gln
 455 460 465
 Ala Ala Ile Tyr Arg Arg Thr Ser Gly Val His Asp Gly Ser Leu
 470 475 480

His Lys Gly Ala Trp Phe Leu Val Cys Ser Gly Ala Leu Val Asn
485 490 495

Glu Arg Thr Val Val Val Ala Ala His Cys Val Thr Asp Leu Gly
500 505 510

Lys Val Thr Met Ile Lys Thr Ala Asp Leu Lys Val Val Leu Gly
515 520 525

Lys Phe Tyr Arg Asp Asp Asp Arg Asp Glu Lys Thr Ile Gln Ser
530 535 540

Leu Gln Ile Ser Ala Ile Ile Leu His Pro Asn Tyr Asp Pro Ile
545 550 555

Leu Leu Asp Ala Asp Ile Ala Ile Leu Lys Leu Leu Asp Lys Ala
560 565 570

Arg Ile Ser Thr Arg Val Gln Pro Ile Cys Leu Ala Ala Ser Arg
575 580 585

Asp Leu Ser Thr Ser Phe Gln Glu Ser His Ile Thr Val Ala Gly
590 595 600

Trp Asn Val Leu Ala Asp Val Arg Ser Pro Gly Phe Lys Asn Asp
605 610 615

Thr Leu Arg Ser Gly Val Val Ser Val Val Asp Ser Leu Leu Cys
620 625 630

Glu Glu Gln His Glu Asp His Gly Ile Pro Val Ser Val Thr Asp
635 640 645

Asn Met Phe Cys Ala Ser Trp Glu Pro Thr Ala Pro Ser Asp Ile
650 655 660

Cys Thr Ala Glu Thr Gly Gly Ile Ala Ala Val Ser Phe Pro Gly
665 670 675

Arg Ala Ser Pro Glu Pro Arg Trp His Leu Met Gly Leu Val Ser
680 685 690

Trp Ser Tyr Asp Lys Thr Cys Ser His Arg Leu Ser Thr Ala Phe
695 700 705

Thr Lys Val Leu Pro Phe Lys Asp Trp Ile Glu Arg Asn Met Lys
710 715 720

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

aggttcgtga tggagacaaac cgcg 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

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<220>
<223> Synthetic oligonucleotide probe

<400> 233
tgtcaaggac gcactgcgt catg 24

<210> 234
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 234
tggccagatc atcaagcgta tctgtggcaa cgagcggcca gtccttatcc 50

<210> 235
<211> 1964
<212> DNA
<213> Homo sapiens

<400> 235
accaggcatt gtatcttcag ttgtcatcaa gttcgaatac agattggaaa 50
agctcaactt gaagctttct tgccgtcagt gaagcagaga gatagatatt 100
attcacgtaa taaaaaacat gggcttcaac ctgactttcc acctttcccta 150
caaattccga ttactgtgc tttttttttt gtgcctgaca gtgggtgggt 200
gggccaccatg taactacttc gtgggtgcata ttcaagagat tcctaaagca 250
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acagttggata tttttttttt gttactgccc taagcagaga gcatgggggt 850
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tgcctgtttt gggtaaatat acaatgggtc tccacactag agacaaaggc 1000
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tgtaaaatgtt ttttgtacaa gtaggatatac aattagcagt ttacaagttt 1900
acatattaaac taataataaaa tatgtctatc aaataacctctt gtagtaaaat 1950
gtgaaaaaagc aaaa 1964

<210> 236

<211> 344

<212> PRT

<213> Homo sapiens

<220>

<221> Signal peptide

<222> 1-27

<223> Signal peptide

<220>

<221> N-glycosylation sites

<222> 4-7, 220-223, 335-338

<223> N-glycosylation sites

<220>

<221> Xylose isomerase proteins

<222> 191-201

<223> Xylose isomerase proteins

<400> 236

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Leu Leu Leu Leu Thr Leu Cys Leu Thr Val Val Gly Trp Ala Thr
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 35 40 45
 Glu Phe Met Ala Asn Phe His Lys Thr Leu Ile Leu Gly Lys Gly
 50 55 60
 Lys Thr Leu Thr Asn Glu Ala Ser Thr Lys Lys Val Glu Leu Asp
 65 70 75
 Asn Cys Pro Ser Val Ser Pro Tyr Leu Arg Gly Gln Ser Lys Leu
 80 85 90
 Ile Phe Lys Pro Asp Leu Thr Leu Glu Glu Val Gln Ala Glu Asn
 95 100 105
 Pro Lys Val Ser Arg Gly Arg Tyr Arg Pro Gln Glu Cys Lys Ala
 110 115 120
 Leu Gln Arg Val Ala Ile Leu Val Pro His Arg Asn Arg Glu Lys
 125 130 135
 His Leu Met Tyr Leu Leu Glu His Leu His Pro Phe Leu Gln Arg
 140 145 150
 Gln Gln Leu Asp Tyr Gly Ile Tyr Val Ile His Gln Ala Glu Gly
 155 160 165
 Lys Lys Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Tyr Leu Glu
 170 175 180
 Ala Leu Lys Glu Glu Asn Trp Asp Cys Phe Ile Phe His Asp Val
 185 190 195
 Asp Leu Val Pro Glu Asn Asp Phe Asn Leu Tyr Lys Cys Glu Glu
 200 205 210
 His Pro Lys His Leu Val Val Gly Arg Asn Ser Thr Gly Tyr Arg
 215 220 225
 Leu Arg Tyr Ser Gly Tyr Phe Gly Gly Val Thr Ala Leu Ser Arg
 230 235 240
 Glu Gln Phe Phe Lys Val Asn Gly Phe Ser Asn Asn Tyr Trp Gly
 245 250 255
 Trp Gly Gly Glu Asp Asp Asp Leu Arg Leu Arg Val Glu Leu Gln
 260 265 270
 Arg Met Lys Ile Ser Arg Pro Leu Pro Glu Val Gly Lys Tyr Thr
 275 280 285
 Met Val Phe His Thr Arg Asp Lys Gly Asn Glu Val Asn Ala Glu
 290 295 300
 Arg Met Lys Leu Leu His Gln Val Ser Arg Val Trp Arg Thr Asp
 305 310 315
 Gly Leu Ser Ser Cys Ser Tyr Lys Leu Val Ser Val Glu His Asn
 320 325 330

Pro Leu Tyr Ile Asn Ile Thr Val Asp Phe Trp Phe Gly Ala
335 340

<210> 237
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 237
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<210> 238
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 238
gagcttcatc cgttctgcgt tcacc 25

<210> 239
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
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<210> 240
<211> 2567
<212> DNA
<213> Homo sapiens

<400> 240
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gcgagactct gtctcca 2567

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<211> 423
<212> PRT
<213> Homo sapiens

<400> 241
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20 25 30
Tyr Glu Leu Asn Leu Thr Thr Asp Ser Pro Ala Thr Thr Gly Ala
35 40 45
Val Val Thr Ile Ser Ala Ser Leu Val Ala Lys Asp Asn Gly Ser
50 55 60
Leu Ala Leu Pro Ala Asp Ala His Leu Tyr Arg Phe His Trp Ile
65 70 75
His Thr Pro Leu Val Leu Thr Gly Lys Met Glu Lys Gly Leu Ser
80 85 90
Ser Thr Ile Arg Val Val Gly His Val Pro Gly Glu Phe Pro Val
95 100 105
Ser Val Trp Val Thr Ala Ala Asp Cys Trp Met Cys Gln Pro Val
110 115 120
Ala Arg Gly Phe Val Val Leu Pro Ile Thr Glu Phe Leu Val Gly
125 130 135
Asp Leu Val Val Thr Gln Asn Thr Ser Leu Pro Trp Pro Ser Ser
140 145 150
Tyr Leu Thr Lys Thr Val Leu Lys Val Ser Phe Leu Leu His Asp
155 160 165
Pro Ser Asn Phe Leu Lys Thr Ala Leu Phe Leu Tyr Ser Trp Asp
170 175 180
Phe Gly Asp Gly Thr Gln Met Val Thr Glu Asp Ser Val Val Tyr
185 190 195

Tyr Asn Tyr Ser Ile Ile Gly Thr Phe Thr Val Lys Leu Lys Val
200 205 210

Val Ala Glu Trp Glu Glu Val Glu Pro Asp Ala Thr Arg Ala Val
215 220 225

Lys Gln Lys Thr Gly Asp Phe Ser Ala Ser Leu Lys Leu Gln Glu
230 235 240

Thr Leu Arg Gly Ile Gln Val Leu Gly Pro Thr Leu Ile Gln Thr
245 250 255

Phe Gln Lys Met Thr Val Thr Leu Asn Phe Leu Gly Ser Pro Pro
260 265 270

Leu Thr Val Cys Trp Arg Leu Lys Pro Glu Cys Leu Pro Leu Glu
275 280 285

Glu Gly Glu Cys His Pro Val Ser Val Ala Ser Thr Ala Tyr Asn
290 295 300

Leu Thr His Thr Phe Arg Asp Pro Gly Asp Tyr Cys Phe Ser Ile
305 310 315

Arg Ala Glu Asn Ile Ile Ser Lys Thr His Gln Tyr His Lys Ile
320 325 330

Gln Val Trp Pro Ser Arg Ile Gln Pro Ala Val Phe Ala Phe Pro
335 340 345

Cys Ala Thr Leu Ile Thr Val Met Leu Ala Phe Ile Met Tyr Met
350 355 360

Thr Leu Arg Asn Ala Thr Gln Gln Lys Asp Met Val Glu Asn Pro
365 370 375

Glu Pro Pro Ser Gly Val Arg Cys Cys Cys Gln Met Cys Cys Gly
380 385 390

Pro Phe Leu Leu Glu Thr Pro Ser Glu Tyr Leu Glu Ile Val Arg
395 400 405

Glu Asn His Gly Leu Leu Pro Pro Leu Tyr Lys Ser Val Lys Thr
410 415 420

Tyr Thr Val

<210> 242

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 242

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<210> 243

<211> 25

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
gaaaaggccca cagcacatct ggcag 25

<210> 244
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 244
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<210> 245
<211> 485
<212> DNA
<213> Homo sapiens

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aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 485

<210> 246
<211> 84
<212> PRT
<213> Homo sapiens

<400> 246

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20 25 30

Thr Gly Gln Leu Ala Glu Leu Gln Pro Gln Asp Arg Ala Gly Ala
35 40 45

Arg Ala Ser Trp Met Pro Met Phe Gln Arg Arg Arg Arg Asp
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Thr His Phe Pro Ile Cys Ile Phe Cys Cys Gly Cys Cys His Arg
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Ser Lys Cys Gly Met Cys Cys Lys Thr
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<210> 247
<211> 2359
<212> DNA
<213> Homo sapiens

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<210> 248
<211> 456
<212> PRT
<213> Homo sapiens

<400> 248
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      20          25          30
Ile Val Pro Ala Ile Phe Gly Val Ser Phe Gly Ile Arg Lys Leu
      35          40          45
Tyr Met Lys Ser Leu Leu Lys Ile Phe Ala Trp Ala Thr Leu Arg
      50          55          60
Met Glu Arg Gly Ala Lys Glu Lys Asn His Gln Leu Tyr Lys Pro
      65          70          75

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Tyr Thr Asn Gly Ile Ile Ala Lys Asp Pro Thr Ser Leu Glu Glu
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Glu Ile Lys Glu Ile Arg Arg Ser Gly Ser Ser Lys Ala Leu Asp
95 100 105
Asn Thr Pro Glu Phe Glu Leu Ser Asp Ile Phe Tyr Phe Cys Arg
110 115 120
Lys Gly Met Glu Thr Ile Met Asp Asp Glu Val Thr Lys Arg Phe
125 130 135
Ser Ala Glu Glu Leu Glu Ser Trp Asn Leu Leu Ser Arg Thr Asn
140 145 150
Tyr Asn Phe Gln Tyr Ile Ser Leu Arg Leu Thr Val Leu Trp Gly
155 160 165
Leu Gly Val Leu Ile Arg Tyr Cys Phe Leu Leu Pro Leu Arg Ile
170 175 180
Ala Leu Ala Phe Thr Gly Ile Ser Leu Leu Val Val Gly Thr Thr
185 190 195
Val Val Gly Tyr Leu Pro Asn Gly Arg Phe Lys Glu Phe Met Ser
200 205 210
Lys His Val His Leu Met Cys Tyr Arg Ile Cys Val Arg Ala Leu
215 220 225
Thr Ala Ile Ile Thr Tyr His Asp Arg Glu Asn Arg Pro Arg Asn
230 235 240
Gly Gly Ile Cys Val Ala Asn His Thr Ser Pro Ile Asp Val Ile
245 250 255
Ile Leu Ala Ser Asp Gly Tyr Tyr Ala Met Val Gly Gln Val His
260 265 270
Gly Gly Leu Met Gly Val Ile Gln Arg Ala Met Val Lys Ala Cys
275 280 285
Pro His Val Trp Phe Glu Arg Ser Glu Val Lys Asp Arg His Leu
290 295 300
Val Ala Lys Arg Leu Thr Glu His Val Gln Asp Lys Ser Lys Leu
305 310 315
Pro Ile Leu Ile Phe Pro Glu Gly Thr Cys Ile Asn Asn Thr Ser
320 325 330
Val Met Met Phe Lys Lys Gly Ser Phe Glu Ile Gly Ala Thr Val
335 340 345
Tyr Pro Val Ala Ile Lys Tyr Asp Pro Gln Phe Gly Asp Ala Phe
350 355 360
Trp Asn Ser Ser Lys Tyr Gly Met Val Thr Tyr Leu Leu Arg Met
365 370 375
Met Thr Ser Trp Ala Ile Val Cys Ser Val Trp Tyr Leu Pro Pro
380 385 390

Met Thr Arg Glu Ala Asp Glu Asp Ala Val Gln Phe Ala Asn Arg
395 400 405
Val Lys Ser Ala Ile Ala Arg Gln Gly Gly Leu Val Asp Leu Leu
410 415 420
Trp Asp Gly Gly Leu Lys Arg Glu Lys Val Lys Asp Thr Phe Lys
425 430 435
Glu Glu Gln Gln Lys Leu Tyr Ser Lys Met Ile Val Gly Asn His
440 445 450
Lys Asp Arg Ser Arg Ser
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<210> 249
<211> 1103
<212> DNA
<213> Homo sapiens

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<210> 250

<211> 240

<212> PRT

<213> Homo sapiens

<400> 250

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20									25					30

Leu	Ala	Pro	Asp	Thr	Phe	Asp	Asp	Thr	Tyr	Val	Gly	Cys	Ala	Glu
35									40					45

Glu	Met	Glu	Glu	Lys	Ala	Ala	Pro	Leu	Leu	Lys	Glu	Glu	Met	Ala
50									55					60

His	His	Ala	Leu	Leu	Arg	Glu	Ser	Trp	Glu	Ala	Ala	Gln	Glu	Thr
65									70					75

Trp	Glu	Asp	Lys	Arg	Arg	Gly	Leu	Thr	Leu	Pro	Pro	Gly	Phe	Lys
80									85					90

Ala	Gln	Asn	Gly	Ile	Ala	Ile	Met	Val	Tyr	Thr	Asn	Ser	Ser	Asn
95									100					105

Thr	Leu	Tyr	Trp	Glu	Leu	Asn	Gln	Ala	Val	Arg	Thr	Gly	Gly	Gly
110									115					120

Ser	Arg	Glu	Leu	Tyr	Met	Arg	His	Phe	Pro	Phe	Lys	Ala	Leu	His
125									130					135

Phe	Tyr	Leu	Ile	Arg	Ala	Leu	Gln	Leu	Leu	Arg	Gly	Ser	Gly	Gly
140									145					150

Cys	Ser	Arg	Gly	Pro	Gly	Glu	Val	Val	Phe	Arg	Gly	Val	Gly	Ser
155									160					165

Leu	Arg	Phe	Glu	Pro	Lys	Arg	Leu	Gly	Asp	Ser	Val	Arg	Leu	Gly
170									175					180

Gln	Phe	Ala	Ser	Ser	Ser	Leu	Asp	Lys	Ala	Val	Ala	His	Arg	Phe
185									190					195

Gly	Glu	Lys	Arg	Arg	Gly	Cys	Val	Ser	Ala	Pro	Gly	Val	Gln	Leu
200									205					210

Gly	Ser	Gln	Ser	Glu	Gly	Ala	Ser	Ser	Leu	Pro	Pro	Trp	Lys	Thr
215									220					225

Leu	Leu	Leu	Ala	Pro	Gly	Glu	Phe	Gln	Leu	Ser	Gly	Val	Gly	Pro
230									235					240

<210> 251

<211> 50

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 252
<211> 1076
<212> DNA
<213> Homo sapiens

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agtgcactcc cctaaaggctc tgctca 1076

<210> 253
<211> 335
<212> PRT
<213> Homo sapiens

<400> 253
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Gly Ser Val Gly Gly Ala Val Thr Phe Pro Leu Lys Ser Lys Val			
35		40	45
Lys Gln Val Asp Ser Ile Val Trp Thr Phe Asn Thr Thr Pro Leu			
50		55	60
Val Thr Ile Gln Pro Glu Gly Gly Thr Ile Ile Val Thr Gln Asn			
65		70	75
Arg Asn Arg Glu Arg Val Asp Phe Pro Asp Gly Gly Tyr Ser Leu			
80		85	90
Lys Leu Ser Lys Leu Lys Lys Asn Asp Ser Gly Ile Tyr Tyr Val			
95		100	105
Gly Ile Tyr Ser Ser Ser Leu Gln Gln Pro Ser Thr Gln Glu Tyr			
110		115	120
Val Leu His Val Tyr Glu His Leu Ser Lys Pro Lys Val Thr Met			
125		130	135
Gly Leu Gln Ser Asn Lys Asn Gly Thr Cys Val Thr Asn Leu Thr			
140		145	150
Cys Cys Met Glu His Gly Glu Glu Asp Val Ile Tyr Thr Trp Lys			
155		160	165
Ala Leu Gly Gln Ala Ala Asn Glu Ser His Asn Gly Ser Ile Leu			
170		175	180
Pro Ile Ser Trp Arg Trp Gly Glu Ser Asp Met Thr Phe Ile Cys			
185		190	195
Val Ala Arg Asn Pro Val Ser Arg Asn Phe Ser Ser Pro Ile Leu			
200		205	210
Ala Arg Lys Leu Cys Glu Gly Ala Ala Asp Asp Pro Asp Ser Ser			
215		220	225
Met Val Leu Leu Cys Leu Leu Leu Val Pro Leu Leu Leu Ser Leu			
230		235	240
Phe Val Leu Gly Leu Phe Leu Trp Phe Leu Lys Arg Glu Arg Gln			
245		250	255
Glu Glu Tyr Ile Glu Glu Lys Lys Arg Val Asp Ile Cys Arg Glu			
260		265	270
Thr Pro Asn Ile Cys Pro His Ser Gly Glu Asn Thr Glu Tyr Asp			
275		280	285
Thr Ile Pro His Thr Asn Arg Thr Ile Leu Lys Glu Asp Pro Ala			
290		295	300
Asn Thr Val Tyr Ser Thr Val Glu Ile Pro Lys Lys Met Glu Asn			
305		310	315
Pro His Ser Leu Leu Thr Met Pro Asp Thr Pro Arg Leu Phe Ala			

320

325

330

Tyr Glu Asn Val Ile
335

<210> 254

<211> 1053

<212> DNA

<213> Homo sapiens

<400> 254

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caagcagcca atgagtccca taatgggtcc atccctccca tctcctggag 550

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cgagaaactt ctcagccccc atccctggca ggaagctctg tgaaggtgct 650

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cgggaaactc ctaacatatg cccccattct ggagagaaca cagagtacga 850

cacaatccct cacactaata gaacaatct aaaggaagat ccagcaaata 900

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ctagacagca gtgcactccc ctaagtctct gctcaaaaaa aaaaaaaaaa 1050

aaa 1053

<210> 255

<211> 860

<212> DNA

<213> Homo sapiens

<400> 255

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gggtctatg gccgagaacc agatttgagt tcagacatca agggaaagggtt 500
tgcacacta tgtgaggagc atggaatcct tagagaaaat atcattgacc 550
tatccaatgc caatcgctgc ctccaggccc gagaatgaag aatggctga 600
gcctccagtg ttgagtgac acttctcacc aggactccac catcatccct 650
tcctatccat acagcatccc cagtataaat tctgtgatct gcattccatc 700
ctgtctcaact gagaagtcca attccagttt atcaacatgt tacctaggat 750
acctcatcaa gaatcaaaga cttctttaaa tttctctttg atacaccctt 800
gacaatttt catgaaattt ttccctttcc tggtaataaa atgattaccc 850
ttgcacttaa 860

<210> 256
<211> 180
<212> PRT
<213> Homo sapiens

<400> 256
Met Lys Met Leu Leu Leu Cys Leu Gly Leu Thr Leu Val Cys
1 5 10 15
Val His Ala Glu Glu Ala Ser Ser Thr Gly Arg Asn Phe Asn Val
20 25 30
Glu Lys Ile Asn Gly Glu Trp His Thr Ile Ile Leu Ala Ser Asp
35 40 45
Lys Arg Glu Lys Ile Glu Glu His Gly Asn Phe Arg Leu Phe Leu
50 55 60
Glu Gln Ile His Val Leu Glu Asn Ser Leu Val Leu Lys Val His
65 70 75
Thr Val Arg Asp Glu Glu Cys Ser Glu Leu Ser Met Val Ala Asp
80 85 90
Lys Thr Glu Lys Ala Gly Glu Tyr Ser Val Thr Tyr Asp Gly Phe
95 100 105
Asn Thr Phe Thr Ile Pro Lys Thr Asp Tyr Asp Asn Phe Leu Met
110 115 120

Ala His Leu Ile Asn Glu Lys Asp Gly Glu Thr Phe Gln Leu Met
125 130

Gly Leu Tyr Gly Arg Glu Pro Asp Leu Ser Ser Asp Ile Lys Glu
140 145 150

Arg Phe Ala Gln Leu Cys Glu Glu His Gly Ile Leu Arg Glu Asn
155 160 165

Ile Ile Asp Leu Ser Asn Ala Asn Arg Cys Leu Gln Ala Arg Glu
170 175 180

<210> 257

<211> 766

<212> DNA

<213> Homo sapiens

<400> 257

ggctcgagcg ttctcgacc aggggtgacc atgacactgt gcgaaggatg 50

gacatcctgc aatggattca gcctgtgtgt tctactgtgt ttaggatgt 100

ttctcaatgc gatacctcta atttgtcgt tagttgagga agaccaattt 150

tctcaaaaacc ccatcttgg ctgttgatgg tggttccag gaattatagg 200

agcaggtctg atggccattc cagaacaac aatgtccctt acagcaagaa 250

aaagagctgtg ctgcaacaac agaactggaa tggtttttc atcattttc 300

agtgtgtatca cagtcattgg tgctgttat tgcatgtga tatccatcca 350

ggctcttta aaaggctctc tcatgtgtaa ttctccaagg aacagtaatg 400

ccatttgcgaa attttcatgg aaaaacatca gtgacattca tccagaatcc 450

ttcaacttgc agtggttttt caatgactct tggtcaccc tcactggttt 500

caataaacc accagtaacg acaccatggc gagttggctgg agagcatcta 550

gtttccactt cgattctgaa gaaaacaac ataggcttat ccacttctca 600

gtattttttag gtctattgtc tggttggatt ctggaggctc tggttggct 650

cagtcagata gtcatcggtt tccttggctc tctgtgtgg a gtctctaagg 700

gaagaagtca aattgtgttag ttaatggga ataaaatgtt agtacgtt 750

gtttgaaaaaa aaaaaa 766

<210> 258

<211> 229

<212> PRT

<213> Homo sapiens

<400> 258

Met Thr Cys Cys Glu Gly Trp Thr Ser Cys Asn Gly Phe Ser Leu
1 5 10 15

Leu Val Leu Leu Leu Gly Val Val Leu Asn Ala Ile Pro Leu
20 25 30

Ile Val Ser Leu Val Glu Glu Asp Gln Phe Ser Gln Asn Pro Ile

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35

40

45

Ser	Cys	Phe	Glu	Trp	Trp	Phe	Pro	Gly	Ile	Ile	Gly	Ala	Gly	Leu
				50					55					60
Met	Ala	Ile	Pro	Ala	Thr	Thr	Met	Ser	Leu	Thr	Ala	Arg	Lys	Arg
				65					70					75
Ala	Cys	Cys	Asn	Asn	Arg	Thr	Gly	Met	Phe	Leu	Ser	Ser	Phe	Phe
			80						85					90
Ser	Val	Ile	Thr	Val	Ile	Gly	Ala	Leu	Tyr	Cys	Met	Leu	Ile	Ser
				95					100					105
Ile	Gln	Ala	Leu	Leu	Lys	Gly	Pro	Leu	Met	Cys	Asn	Ser	Pro	Ser
			110						115					120
Asn	Ser	Asn	Ala	Asn	Cys	Glu	Phe	Ser	Leu	Lys	Asn	Ile	Ser	Asp
			125						130					135
Ile	His	Pro	Glu	Ser	Phe	Asn	Leu	Gln	Trp	Phe	Phe	Asn	Asp	Ser
			140						145					150
Cys	Ala	Pro	Pro	Thr	Gly	Phe	Asn	Lys	Pro	Thr	Ser	Asn	Asp	Thr
			155						160					165
Met	Ala	Ser	Gly	Trp	Arg	Ala	Ser	Ser	Phe	His	Phe	Asp	Ser	Glu
			170						175					180
Glu	Asn	Lys	His	Arg	Leu	Ile	His	Phe	Ser	Val	Phe	Leu	Gly	Leu
			185						190					195
Leu	Leu	Val	Gly	Ile	Leu	Glu	Val	Leu	Phe	Gly	Leu	Ser	Gln	Ile
			200						205					210
Val	Ile	Gly	Phe	Leu	Gly	Cys	Leu	Cys	Gly	Val	Ser	Lys	Arg	Arg
			215						220					225
Ser	Gln	Ile	Val											

<210> 259

<211> 434

<212> DNA

<213> Homo sapiens

<400> 259

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caccatgagg ctgtcagtgt gtctcctgtat ggtctcgctg gccctttgc 100
gctaccaggg ccatgcttgc gtctgccag ctgttgcttc tgagatcaca 150
gtcttcattat tcttaagtga cgctgcggta aacctccaag ttgccaaact 200
taatccacctt ccagaagctc ttgcagccaa gttggaaagtgc aagcactgca 250
ccgatcagat atcttttaag aaacgactct cattgaaaaaa gtccctggtgg 300
aaatagtgaaa aaaaatgtggt gtgtgacatg taaaaatgtcaaacgtgg 350
tcctaaaggct ttcaacgaca ccctgatctt cactaaaaat tgtaaagggtt 400

tcaacacgtt gcttaataa atcacttgcc ctgc 434

<210> 260

<211> 83

<212> PRT

<213> Homo sapiens

<400> 260

Met	Arg	Leu	Ser	Val	Cys	Leu	Leu	Met	Val	Ser	Leu	Ala	Leu	Cys
1				5					10					15

Cys	Tyr	Gln	Ala	His	Ala	Leu	Val	Cys	Pro	Ala	Val	Ala	Ser	Glu
				20				25						30

Ile	Thr	Val	Phe	Leu	Phe	Leu	Ser	Asp	Ala	Ala	Val	Asn	Leu	Gln
								35			40			45

Val	Ala	Lys	Leu	Asn	Pro	Pro	Pro	Glu	Ala	Leu	Ala	Ala	Lys	Leu
				50					55					60

Glu	Val	Lys	His	Cys	Thr	Asp	Gln	Ile	Ser	Phe	Lys	Lys	Arg	Leu
				65					70					75

Ser	Leu	Lys	Lys	Ser	Trp	Trp	Lys							
				80										

<210> 261

<211> 636

<212> DNA

<213> Homo sapiens

<400> 261

atccggttctc tgcgctgcc a gtcaggta gcccctgcc a aggtgaccc 50

gcaggacact ggtgaaggag cagtggaa cctgcagagt cacacagttg 100

ctgaccatt gagctgttag cctggagca g atccgtggc tgcatggcccc 150

cgc cccca gtc ctccccc tgcagccctg cccctcgaa t gtc acatgg 200

agagagttag cctggccctt ctcc tactgg caggcctgac tgccttggaa 250

gccaatgacc catttgc ccaa taaa gac gat cccttctact atgacttggaa 300

aaacctgc a ctgagccgac t gatctgc gg gctctg gccatttgc t 350

ggatcgcggc agttctgat g gca aat gca aataca aag cagccaga aag 400

cagcacatgc ctgtac tgc a gaggccatc ccactcatca ctccaggctc 450

tgccactact tgctgagc ac ggactggcc tccaggatg gcttga ggc 500

taa acttggc cccca gacc tcc tccctg ggaggc tta tcc tca a gga 550

aggacttctc tccaagg gca ggctttagg ccccttctg atcaggaggc 600

ttctttatga attaaactcg cccca cacc acc ccctca 636

<210> 262

<211> 89

<212> PRT

<213> Homo sapiens

<400> 262
Met Glu Arg Val Thr Leu Ala Leu Leu Leu Ala Gly Leu Thr
1 5 10 15
Ala Leu Glu Ala Asn Asp Pro Phe Ala Asn Lys Asp Asp Pro Phe
20 25 30
Tyr Tyr Asp Trp Lys Asn Leu Gln Leu Ser Gly Leu Ile Cys Gly
35 40 45
Gly Leu Leu Ala Ile Ala Gly Ile Ala Ala Val Leu Ser Gly Lys
50 55 60
Cys Lys Tyr Lys Ser Ser Gln Lys Gln His Ser Pro Val Pro Glu
65 70 75
Lys Ala Ile Pro Leu Ile Thr Pro Gly Ser Ala Thr Thr Cys
80 85

<210> 263
<211> 1676
<212> DNA
<213> Homo sapiens

<400> 263
ggagaagagg ttgtgtggg caagctgctc ccgcacagaag gatgtcgctg 50
ctgagccctgc cctggctggg cctcagaccg gtggcaatgt ccccatggct 100
actcctgtgt ctgggtgtgg gtcctctggc actcgccccg atcctggctt 150
ggaccttatgc ctctataac aactgcgcgc ggctccagtg tttcccacag 200
cccccaaaac ggaactgtt ttggggtaac ctggccctga tcactctac 250
agaggaggggc ttgaaggact cgacccagat gtggccacc tattccagg 300
gtttacggt atggctggg cccatcatcc ctttcatcg tttatggcac 350
cctgacacca tccggcttat caccaatgcc tcagctgcac ttgcacccaa 400
ggataatctc ttcatcagg tccctgaagcc ctggctgggaa gaaggatac 450
tgctgatggg cgggtacacag tggagccccc accgtcgat gctgacgccc 500
gccttcatt tcaacatccat gaagtccatat ataacgatct tcaacaagag 550
tgcaaacatc atgcttgaca agtggcagca cttggccctca gagggcagca 600
gtcgtctggg catgtttag cacaatcaggc tcatgacccat ggacagtcta 650
cagaaatgca tcttcagctt tgacagccat tgcaggaga ggcccagtga 700
atataattgcc accatcttgg agctcagtgc ctttgtagag aaaagaagcc 750
agcatatccct ccacgacatc gactttctgtt attacctctc ccatgacggg 800
cgccgcctcc acaggggctc cccgcctgggtt catgacttca cagacgctgt 850
catccggag cggcgtcgca ccctcccccac tcagggattt gatgatTTT 900
teaaagacaa agccaagttcc aagactttgg atttcatttga ttttgtttctg 950

ctgagcaagg atgaagatgg gaaggcattt ttagatgagg atataagagc 1000
 agaggctgac accttcatgt ttggaggcca tgacaccacg gccagtggcc 1050
 tctcctgggt cctgtacaac cttgcgagcc acccagaata ccaggagcgc 1100
 tggcgacagg aggttcaaga gcttctgaag gaccgcgatc ctaaaagat 1150
 tgaatggac gacctggccc agctgcctt cctgaccatg tgcgtgaagg 1200
 agagcctgag gttacatccc ccagctccct tcatctcccg atgctgcacc 1250
 caggacattt ttctcccaaga tggccgagtc atccccaaag gcattacgt 1300
 cctcatcgat attatagggg tccatcacaa cccaaactgtg tggccggatc 1350
 ctgaggctca cgacccttc cgctttgacc cagagaacacg caaggggagg 1400
 tcacacttgg cttttattcc ttctccgca gggcccgaga actgcacatgg 1450
 gcaggcggtc gccatggcg agatgaaagt ggtcctggcg ttgatgctgc 1500
 tgcacttccg gttoctgcga gaccacactg agcccccgag gaagctggaa 1550
 ttgatcatgc ggcggcgagg cgggcttgg ctgcgggtgg agccctgaa 1600
 ttaggcttg cagtgaacctt ctgaccatc cacctgtttt tttgcagatt 1650
 gtcatgaata aaacgggtct gtcaaa 1676

<210> 264
 <211> 524
 <212> PRT
 <213> Homo sapiens

<400>	264																																																		
Met Ser Leu Leu Ser Leu Pro Trp Leu Gly Leu Arg Pro Val Ala																																																			
1	5	10	15	Met Ser Pro Trp Leu Leu Leu Leu Val Val Gly Ser Trp Leu		20	25	30		Leu Ala Arg Ile Leu Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys		35	40	45		Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe		50	55	60		Trp Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys		65	70	75		Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val		80	85	90		Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp		95	100	105		Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys		110	115	120		Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly		125	130	135	
10	15																																																		
Met Ser Pro Trp Leu Leu Leu Leu Val Val Gly Ser Trp Leu																																																			
20	25	30		Leu Ala Arg Ile Leu Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys		35	40	45		Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe		50	55	60		Trp Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys		65	70	75		Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val		80	85	90		Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp		95	100	105		Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys		110	115	120		Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly		125	130	135							
30																																																			
Leu Ala Arg Ile Leu Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys																																																			
35	40	45		Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe		50	55	60		Trp Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys		65	70	75		Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val		80	85	90		Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp		95	100	105		Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys		110	115	120		Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly		125	130	135													
45																																																			
Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe																																																			
50	55	60		Trp Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys		65	70	75		Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val		80	85	90		Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp		95	100	105		Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys		110	115	120		Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly		125	130	135																			
60																																																			
Trp Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys																																																			
65	70	75		Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val		80	85	90		Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp		95	100	105		Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys		110	115	120		Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly		125	130	135																									
75																																																			
Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val																																																			
80	85	90		Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp		95	100	105		Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys		110	115	120		Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly		125	130	135																															
90																																																			
Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp																																																			
95	100	105		Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys		110	115	120		Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly		125	130	135																																					
105																																																			
Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys																																																			
110	115	120		Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly		125	130	135																																											
120																																																			
Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly																																																			
125	130	135																																																	
135																																																			

Ile	Leu	Leu	Ser	Gly	Gly	Asp	Trp	Ser	Arg	His	Arg	Arg	Met	
													140	
													145	
Leu	Thr	Pro	Ala	Phe	His	Phe	Asn	Ile	Leu	Lys	Ser	Tyr	Ile	Thr
													155	160
														165
Ile	Phe	Asn	Lys	Ser	Ala	Asn	Ile	Met	Leu	Asp	Lys	Trp	Gln	His
													170	175
														180
Leu	Ala	Ser	Glu	Gly	Ser	Ser	Arg	Leu	Asp	Met	Phe	Glu	His	Ile
													185	190
														195
Ser	Leu	Met	Thr	Leu	Asp	Ser	Leu	Gln	Lys	Cys	Ile	Phe	Ser	Phe
													200	205
														210
Asp	Ser	His	Cys	Gln	Glu	Arg	Pro	Ser	Glu	Tyr	Ile	Ala	Thr	Ile
													215	220
														225
Leu	Glu	Leu	Ser	Ala	Leu	Val	Glu	Lys	Arg	Ser	Gln	His	Ile	Leu
													230	235
														240
Gln	His	Met	Asp	Phe	Leu	Tyr	Tyr	Leu	Ser	His	Asp	Gly	Arg	Arg
													245	250
														255
Phe	His	Arg	Ala	Cys	Arg	Leu	Val	His	Asp	Phe	Thr	Asp	Ala	Val
													260	265
														270
Ile	Arg	Glu	Arg	Arg	Arg	Thr	Leu	Pro	Thr	Gln	Gly	Ile	Asp	Asp
													275	280
														285
Phe	Phe	Lys	Asp	Lys	Ala	Lys	Ser	Lys	Thr	Leu	Asp	Phe	Ile	Asp
													290	295
														300
Val	Leu	Leu	Leu	Ser	Lys	Asp	Glu	Asp	Gly	Lys	Ala	Leu	Ser	Asp
													305	310
														315
Glu	Asp	Ile	Arg	Ala	Glu	Ala	Asp	Thr	Phe	Met	Phe	Gly	Gly	His
													320	325
														330
Asp	Thr	Thr	Ala	Ser	Gly	Leu	Ser	Trp	Val	Leu	Tyr	Asn	Leu	Ala
													335	340
														345
Arg	His	Pro	Glu	Tyr	Gln	Glu	Arg	Cys	Arg	Gln	Glu	Val	Gln	Glu
													350	355
														360
Leu	Leu	Lys	Asp	Arg	Asp	Pro	Lys	Glu	Ile	Glu	Trp	Asp	Asp	Leu
													365	370
														375
Ala	Gln	Leu	Pro	Phe	Leu	Thr	Met	Cys	Val	Lys	Glu	Ser	Leu	Arg
													380	385
														390
Leu	His	Pro	Pro	Ala	Pro	Phe	Ile	Ser	Arg	Cys	Cys	Thr	Gln	Asp
													395	400
														405
Ile	Val	Leu	Pro	Asp	Gly	Arg	Val	Ile	Pro	Lys	Gly	Ile	Thr	Cys
													410	415
														420
Leu	Ile	Asp	Ile	Ile	Gly	Val	His	His	Asn	Pro	Thr	Val	Trp	Pro
													425	430
														435
Asp	Pro	Glu	Val	Tyr	Asp	Pro	Phe	Arg	Phe	Asp	Pro	Glu	Asn	Ser
													440	445
														450

Lys Gly Arg Ser Pro Leu Ala Phe Ile Pro Phe Ser Ala Gly Pro
455 460 465
Arg Asn Cys Ile Gly Gln Ala Phe Ala Met Ala Glu Met Lys Val
470 475 480
Val Leu Ala Leu Met Leu Leu His Phe Arg Phe Leu Pro Asp His
485 490 495
Thr Glu Pro Arg Arg Lys Leu Glu Leu Ile Met Arg Ala Glu Gly
500 505 510
Gly Leu Trp Leu Arg Val Glu Pro Leu Asn Val Gly Leu Gln
515 520

<210> 265
<211> 584
<212> DNA
<213> Homo sapiens

<400> 265
caacagaagc caagaaggaa gccgtctatc ttgtggcgat catgtataag 50
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tcttcctctc cttgactcca gggaaatatac ctttcaactc tcagcacctc 150
atgaagacgc ggcgttaact ccggaggaggc tagaaagagc ttcccttcta 200
cagatattgc cagagatgtc gggtgagaa agagggata ttctcaggaa 250
agcagactca agtaccaaca ttttaaccc aagaggaaat ttgagaaagt 300
ttcaggattt ctctggacaa gatcctaaca ttttacttgtc tcatcttttg 350
gccagaatctt gggaaaccata caagaaacgt gagactctg attgcttctg 400
gaaatactgt gtctgaatgt aaataagcat ctgttagtca gctcagaaac 450
accatctta gaatatgaaa aataacacaa tgcttgattt gaaaacgtg 500
tggagaaaaaa cttagccaaac tacaccctgt tcattgttac ctggaaaata 550
aatcccttat gttttgcaca aaaaaaaaaa aaaa 584

<210> 266
<211> 124
<212> PRT
<213> Homo sapiens

<400> 266
Met Tyr Lys Leu Ala Ser Cys Cys Leu Leu Phe Thr Gly Phe Leu
1 5 10 15
Asn Pro Leu Leu Ser Leu Pro Leu Leu Asp Ser Arg Glu Ile Ser
20 25 30
Phe Gln Leu Ser Ala Pro His Glu Asp Ala Arg Leu Thr Pro Glu
35 40 45
Glu Leu Glu Arg Ala Ser Leu Leu Gln Ile Leu Pro Glu Met Leu
50 55 60

Gly Ala Glu Arg Gly Asp Ile Leu Arg Lys Ala Asp Ser Ser Thr
65 70 75
Asn Ile Phe Asn Pro Arg Gly Asn Leu Arg Lys Phe Gln Asp Phe
80 85 90
Ser Gly Gln Asp Pro Asn Ile Leu Leu Ser His Leu Leu Ala Arg
95 100 105
Ile Trp Lys Pro Tyr Lys Lys Arg Glu Thr Pro Asp Cys Phe Trp
110 115 120
Lys Tyr Cys Val

<210> 267
<211> 654
<212> DNA
<213> Homo sapiens

<400> 267
gaacatttt agttcccaag gaatgtacat cagccccaaag gaagcttaggc 50
cacctctggg atgggggttc tggtttaaaa caaacgccag tcatcctata 100
taaggacactg acagccacca ggcaccacct ccggcaggaa ctgcaggccc 150
acctgtctgc aaccctgatc agggccatgcc ctcccccaggg accgtctgca 200
gcctctgtc cctcggtatc ctctggctgg acttggcatc ggcaggctcc 250
agcttctgtc gcccgtaca ccagagatc cagcagagaa aggagtgc 300
gaagccacca gccaagctgc agcccccggc tctagcaggc tggctccggc 350
cggaagatgg aggtcaagca gaagggggcag aggtatggactt ggaagtccgg 400
ttcaacgc cctttgtatc tggatcaag ctgtcagggg ttcatgtacca 450
gcagcacacg caggccctgg ggaagtttc tcaggacatc ctctggaaag 500
aggccaaaga ggcggccggc gacaagtgtatc cgccacaag ctttactcac 550
ctctctctaa gtttagaagc gctcatgtgg ctttcgctt gcttctgcag 600
caactccac gactgttgta caagctcagg aggccataaa atgttcaaac 650
tgta 654

<210> 268
<211> 117
<212> PRT
<213> Homo sapiens

<400> 268
Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Leu Gly Met
1 5 10 15
Leu Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro
20 25 30
Glu His Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro
35 40 45

Ala Lys Leu Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu
50 55 60
Asp Gly Gly Gln Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg
65 70 75
Phe Asn Ala Pro Phe Asp Val Gly Ile Lys Leu Ser Gly Val Gln
80 85 90
Tyr Gln Gln His Ser Gln Ala Leu Gly Lys Phe Leu Gln Asp Ile
95 100 105
Leu Trp Glu Ala Lys Glu Ala Pro Ala Asp Lys
110 115

<210> 269
<211> 1332
<212> DNA
<213> Homo sapiens

<400> 269
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cagccccgtta tagtcgtgtat catcggatgc ctctgtgtcc tgctggactt 200
tcttggcttg gtgcacccgtt gccagctgtat catcttccac atcttacactga 250
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cacgcctggg gccagagtct ttgtcccccgt tttgcgcatt tggtcagggt 400
cagcctctcc cagaaggtagt atcatggaca aaaaggccaa atcacaggaa 450
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aaatataattt caggcaggatcc acccactaacaa caaacaactg aagcgagac 700
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 cgcataatctt acagtcactg ttgtcttgcc tgagggttga atttttttta 1250
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1332

<210> 270
<211> 142
<212> PRT
<213> Homo sapiens

<400> 270
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 Gln Thr Leu Ile Val Val Ile Ile Gly Met Leu Val Leu Leu Leu
 20 25 30
 Asp Phe Leu Gly Leu Val His Leu Gly Gln Leu Leu Ile Phe His
 35 40 45
 Ile Tyr Leu Ser Met Ser Pro Thr Leu Ser Pro Arg Ser Pro Gln
 50 55 60
 Gly Trp Val Val Arg Ala Ala His Leu Thr Pro Leu Leu Glu Tyr
 65 70 75
 Val Pro Asn Pro Glu Pro Pro Thr Pro Gly Ala Arg Val Phe Val
 80 85 90
 Pro Arg Val Arg Met Cys Ser Gly Ser Ala Ser Pro Arg Ser Glu
 95 100 105
 Ile Met Asp Lys Lys Gly Lys Ser Gln Glu Glu Ile Lys Ser Met
 110 115 120
 Arg Thr Gln Gln Ala Gln Gln Glu Ala Glu Leu Thr Pro Arg Pro
 125 130 135
 Ala Gly Val Val Pro Gly Ala
 140

<210> 271
<211> 1484
<212> DNA
<213> Homo sapiens

<400> 271
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 cctatatgtcc atcctcagca tgctatcact cagcttctcc acaacatccc 150
 tgctcagcaa ctactggttt gtgggcacac agaagggtgcc caagccccctg 200
 tgcgagaaag gtctggcagc caagtgcattt gacatgccag tgtccctggaa 250

099154
tggagatacc aacacatcca cccaggaggt ggtacaatac aactgggaga 300
ctgggatga ccggcttc tccggagct tccggagtgg catgtggcta 350
tcctgtgagg aaactgtgga agaaccaggg gagaggtgcc gaagtttcat 400
tgaacttaca ccaccagcca agagaggtga gaaaggacta ctggaatttg 450
ccacgttgc agggccatgt cacccactc tccgatttg aggaaagcg 500
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cggtgtcac cacctcaac acgtacacca ggatggtgct ggagttcaag 900
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cttggttcac ccacccacca ttcacacat ccagaattcc cttctttact 1400
gatagtttct gtgccaggtt ctgggctaaa ccatggagat aaaaagaaga 1450
gtaaaataca ctcccgacc ttaaggatct gaaa 1484

<210> 272

<211> 285

<212> PRT

<213> Homo sapiens

<400> 272

Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln Arg Thr

1

5

10

15

Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser Thr

20

25

30

Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val

35	40	45
Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp		
50	55	60
Met Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu		
65	70	75
Val Val Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe		
80	85	90
Arg Ser Phe Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val		
95	100	105
Glu Glu Pro Gly Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro		
110	115	120
Pro Ala Lys Arg Gly Glu Lys Gly Leu Leu Glu Phe Ala Thr Leu		
125	130	135
Gln Gly Pro Cys His Pro Thr Leu Arg Phe Gly Gly Lys Arg Leu		
140	145	150
Met Glu Lys Ala Ser Leu Pro Ser Pro Pro Leu Gly Leu Cys Gly		
155	160	165
Lys Asn Pro Met Val Ile Pro Gly Asn Ala Asp His Leu His Arg		
170	175	180
Thr Ser Ile His Gln Leu Pro Pro Ala Thr Asn Arg Leu Ala Thr		
185	190	195
His Trp Glu Pro Cys Leu Trp Ala Gln Thr Glu Arg Leu Cys Cys		
200	205	210
Cys Phe Leu Cys Pro Val Arg Ser Pro Gly Asp Gly Gly Pro His		
215	220	225
Asp Val Phe Thr Ser Leu Pro Ser Asp Cys Gln Leu Gly Ser Arg		
230	235	240
Arg Leu Glu Thr Cys Leu Glu Leu Trp Leu Gly Leu Leu His		
245	250	255
Gly Leu Ala Leu Leu His Leu Leu His Gly Val Gly Cys His His		
260	265	270
Leu Gln His Val His Gln Asp Gly Ala Gly Val Gln Val Gln Ala		
275	280	285

<210> 273
<211> 1158
<212> DNA
<213> Homo sapiens

<400> 273
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ctctggtagc cttcagagca aacaggacaa cctatgttat ggatgtttcc 200

accaaccagg gtagtggcat ggagcacccgt aaccatctgt gcttcgtgta 250
tctctatgac agagccactt ctccacccct gaaatgtcc ctgcctctgaa 300
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cctgcccata tccctctccc aagtctgttc tcttattgtc aacctcagca 400
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accccccgtg cagccagtagt taacatgtcc ccttccccct gcggcccg 550
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cagcctccccc gtagccatct ccagggtgac ggaacccagt gtattacgt 1050
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tttctccaaat tatgccccatg ccacccaaaac aataaaacaa aattctctaa 1150
cactgaaa 1158

<210> 274
<211> 86
<212> PRT
<213> Homo sapiens

<400> 274

Met	Trp	Leu	Pro	Leu	Gly	Leu	Leu	Ser	Leu	Cys	Leu	Ser	Pro	Leu
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Pro Ile Leu Ser Ser Pro Ser Leu Lys Ser Gln Ala Cys Gln Gln
20 25 30

Leu Leu Trp Thr Leu Pro Ser Pro Leu Val Ala Phe Arg Ala Asn
35 40 45

Arg Thr Thr Tyr Val Met Asp Val Ser Thr Asn Gln Gly Ser Gly
50 55 60

Met Glu His Arg Asn His Leu Cys Phe Cys Asp Leu Tyr Asp Arg
65 70 75

Ala Thr Ser Pro Pro Leu Lys Cys Ser Leu Leu
80 85

<210> 275
<211> 2694
<212> DNA
<213> *Homo sapiens*

卷之三

<210> 276

<211> 131

<212> PRT

<213> Homo sapiens

<400> 276

Met Ala Gly Ile Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala
1 5 10 15

Ile Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr
20 25 30

Asn Lys Tyr Trp Pro Leu Phe Val Leu Phe Phe Tyr Ile Leu Ser

35

40

45

Pro Ile Pro Tyr Cys Ile Ala Arg Arg Leu Val Asp Asp Thr Asp		
50	55	60
Ala Met Ser Asn Ala Cys Lys Glu Leu Ala Ile Phe Leu Thr Thr		
65	70	75
Gly Ile Val Val Ser Ala Phe Gly Leu Pro Ile Val Phe Ala Arg		
80	85	90
Ala His Leu Ile Glu Trp Gly Ala Cys Ala Leu Val Leu Thr Gly		
95	100	105
Asn Thr Val Ile Phe Ala Thr Ile Leu Gly Phe Phe Leu Val Phe		
110	115	120

Gly Ser Asn Asp Asp Phe Ser Trp Gln Gln Trp		
125	130	

<210> 277

<211> 4104

<212> DNA

<213> Homo sapiens

<400> 277

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cgccgcgcgtc cgcacccccc caaccgcgcg cggccgcgcg cggccgcgcg 200		
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gtca 4104

<210> 278
<211> 522
<212> PRT
<213> Homo sapiens

<400> 278

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			20				25					30		
Met	Leu	Pro	Ala	Ala	Pro	Ser	Gly	Cys	Pro	Gln	Leu	Cys	Arg	Cys
	35							40				45		
Glu	Gly	Arg	Leu	Leu	Tyr	Cys	Glu	Ala	Leu	Asn	Leu	Thr	Glu	Ala
			50					55				60		
Pro	His	Asn	Leu	Ser	Gly	Leu	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn
	65							70				75		
Ser	Leu	Ser	Glu	Leu	Arg	Ala	Gly	Gln	Phe	Thr	Gly	Leu	Met	Gln
	80							85				90		
Leu	Thr	Trp	Leu	Tyr	Leu	Asp	His	Asn	His	Ile	Cys	Ser	Val	Gln
	95							100				105		
Gly	Asp	Ala	Phe	Gln	Lys	Leu	Arg	Arg	Val	Lys	Glu	Leu	Thr	Leu
	110							115				120		
Ser	Ser	Asn	Gln	Ile	Thr	Gln	Leu	Pro	Asn	Thr	Thr	Phe	Arg	Pro
	125							130				135		
Met	Pro	Asn	Leu	Arg	Ser	Val	Asp	Leu	Ser	Tyr	Asn	Lys	Leu	Gln
	140							145				150		
Ala	Leu	Ala	Pro	Asp	Leu	Phe	His	Gly	Leu	Arg	Lys	Leu	Thr	Thr
	155							160				165		
Leu	His	Met	Arg	Ala	Asn	Ala	Ile	Gln	Phe	Val	Pro	Val	Arg	Ile
	170							175				180		
Phe	Gln	Asp	Cys	Arg	Ser	Leu	Lys	Phe	Leu	Asp	Ile	Gly	Tyr	Asn
	185							190				195		
Gln	Leu	Lys	Ser	Leu	Ala	Arg	Asn	Ser	Phe	Ala	Gly	Leu	Phe	Lys
	200							205				210		
Leu	Thr	Glu	Leu	His	Leu	Glu	His	Asn	Asp	Leu	Val	Lys	Val	Asn
	215							220				225		
Phe	Ala	His	Phe	Pro	Arg	Leu	Ile	Ser	Leu	His	Ser	Leu	Cys	Leu
	230							235				240		
Arg	Arg	Asn	Lys	Val	Ala	Ile	Val	Val	Ser	Ser	Leu	Asp	Trp	Val
	245							250				255		
Trp	Asn	Leu	Glu	Lys	Met	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Tyr
	260							265				270		
Met	Glu	Pro	His	Val	Phe	Glu	Thr	Val	Pro	His	Leu	Gln	Ser	Leu
	275							280				285		

Gln Leu Asp Ser Asn Arg Leu Thr Tyr Ile Glu Pro Arg Ile Leu
290 295 300
Asn Ser Trp Lys Ser Leu Thr Ser Ile Thr Leu Ala Gly Asn Leu
305 310 315
Trp Asp Cys Gly Arg Asn Val Cys Ala Leu Ala Ser Trp Leu Ser
320 325 330
Asn Phe Gln Gly Arg Tyr Asp Gly Asn Leu Gln Cys Ala Ser Pro
335 340 345
Glu Tyr Ala Gln Gly Glu Asp Val Leu Asp Ala Val Tyr Ala Phe
350 355 360
His Leu Cys Glu Asp Gly Ala Glu Pro Thr Ser Gly His Leu Leu
365 370 375
Ser Ala Val Thr Asn Arg Ser Asp Leu Gly Pro Pro Ala Ser Ser
380 385 390
Ala Thr Thr Leu Ala Asp Gly Gly Glu Gly Gln His Asp Gly Thr
395 400 405
Phe Glu Pro Ala Thr Val Ala Leu Pro Gly Gly Glu His Ala Glu
410 415 420
Asn Ala Val Gln Ile His Lys Val Val Thr Gly Thr Met Ala Leu
425 430 435
Ile Phe Ser Phe Leu Ile Val Val Leu Val Leu Tyr Val Ser Trp
440 445 450
Lys Cys Phe Pro Ala Ser Leu Arg Gln Leu Arg Gln Cys Phe Val
455 460 465
Thr Gln Arg Arg Lys Gln Lys Gln Lys Gln Thr Met His Gln Met
470 475 480
Ala Ala Met Ser Ala Gln Glu Tyr Tyr Val Asp Tyr Lys Pro Asn
485 490 495
His Ile Glu Gly Ala Leu Val Ile Ile Asn Glu Tyr Gly Ser Cys
500 505 510
Thr Cys His Gln Gln Pro Ala Arg Glu Cys Glu Val
515 520

<210> 279

<211> 46

<212> DNA

<213> Artificial Sequence

<220> 279

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<210> 280

<211> 709

<212> DNA

<213> Homo sapiens

<400> 280
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 ccggcgccgc cggttagtgc ccggggaca agatgggtgc agtccgtgtc 200
 caagaaggtc acgcccgtctc agacatgctc ctggcgctgg atgggaaact 250
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 ggccggggcgcg gctgagcggtg ggccccgagg actgcgcgga cccgtggc 650
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<210> 281

<211> 229
<212> PRT
<213> Homo sapiens

<400> 281
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 20 25 30
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 35 40 45
 Gly Ala Val Glu Phe Pro Ala Asp Lys Met Val Ser Val Leu Val
 50 55 60
 Gln Glu Gly His Ala Val Ser Asp Met Leu Leu Pro Leu Asp Gly
 65 70 75
 Glu Leu Val Leu Ala Ser Gly Ala Gly Phe Gly Val Ser Asp Val
 80 85 90
 Gly Ser His Leu Asp Cys Gly Ala Gly Glu Pro Ala Val Phe Arg
 95 100 105
 Asp Ser Asp Arg Phe Ser Trp His Asp Pro His Leu Trp Arg Ser
 110 115 120
 Gly Asp Glu Ala Pro Gly Leu Phe Phe Val Asp Ala Glu Arg Val
 125 130 135

Pro	Cys	Arg	His	Asp	Asp	Val	Phe	Phe	Pro	Pro	Ser	Ala	Ser	Phe
						140			145					150
Arg	Val	Gly	Leu	Gly	Pro	Gly	Ala	Ser	Pro	Val	Arg	Val	Arg	Ser
					155				160					165
Ile	Ser	Ala	Leu	Gly	Arg	Thr	Phe	Thr	Arg	Asp	Glu	Asp	Leu	Ala
					170				175					180
Val	Phe	Leu	Ala	Ser	Arg	Ala	Gly	Arg	Leu	Arg	Phe	His	Gly	Pro
					185				190					195
Gly	Ala	Leu	Ser	Val	Gly	Pro	Glu	Asp	Cys	Ala	Asp	Pro	Ser	Gly
				200					205					210
Cys	Val	Cys	Gly	Asn	Ala	Glu	Ala	Gln	Pro	Trp	Ile	Cys	Ala	Ala
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Leu Leu Gln Pro

<210> 282
<211> 644
<212> DNA
<213> *Homo sapiens*

<400> 282
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ttggcagaaatg ctgggtggaca gttttgtaac tatcttcgaa acctctgtct 350
tacagacatg tgccttttat cttgcagcaa tgtgttgctt gtgattcgaa 400
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aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaa 644

<210> 283
<211> 77
<212> PRT
<213> *Homo sapiens*

<400> 283
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Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr Leu

20

25

30

Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe
 35 40 45

Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe
50 55 60

Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys
65 70 75

Leu Ala

<210> 284
<211> 2623
<212> DNA
<213> *Homo sapiens*

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gctgtatgaag ggtggcacat ttacagaat aagttagatg actttctgtt 1250
aggcaaccac ggttacgata atgcgttagc agatatgcat ccaatatttt 1300
tagccccatgg tcctgccttc agaaaattt tctcaaaaaga agccatgaac 1350
tccacagatt tgcgttccact actatgccac ctccctcaata tcactgccc 1400
gccacacaat ggatcattct ggaatgtcca ggatctgtc aattcagcaa 1450
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gtttaaccag cagaatatga ccaagagggg tcataccctt atttcattagg 1550
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tatttggatgtt gagattccat aattatgtca gtgtttaaag gtttcaattt 1750
ctggaaacc agttccaaac atctgcagaa accattaagc agttacatata 1800
ttaggtaatac acacacacac acacacacac atacacacac acggccaaa 1850
atacttacac ctgcaaaaggaa ataaagatgtt gagatgttgc ctccattgtt 1900
cactgttagca tagggataga taagatcctt cttttatttttggacttggcgca 1950
gataatgtat atattttagca actttgcact atgttaaagta ctttatatat 2000
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atggacagt atgtcttata acttggattga aaatgacaac tttttgcacc 2100
catgtcacaac aataacttggt acgcattgtt caaaactgaaag gaaatttcta 2150
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ggataaaaaaa aaaaaaaaaaaa aaa 2623

<210> 285

<211> 477
<212> PRT
<213> Homo sapiens

<400> 285
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20 25 30
Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asp Tyr Leu Tyr Lys
35 40 45
Val Pro Thr Pro His Phe His Tyr Ile Met Lys Tyr Gly Val His
50 55 60
Val Lys Gln Val Thr Asn Val Phe Ile Thr Lys Thr Tyr Pro Asn
65 70 75
His Tyr Thr Leu Val Thr Gly Leu Phe Ala Glu Asn His Gly Ile
80 85 90
Val Ala Asn Asp Met Phe Asp Pro Ile Arg Asn Lys Ser Phe Ser
95 100 105
Leu Asp His Met Asn Ile Tyr Asp Ser Lys Phe Trp Glu Glu Ala
110 115 120
Thr Pro Ile Trp Ile Thr Asn Gln Arg Ala Gly His Thr Ser Gly
125 130 135
Ala Ala Met Trp Pro Gly Thr Asp Val Lys Ile His Lys Arg Phe
140 145 150
Pro Thr His Tyr Met Pro Tyr Asn Glu Ser Val Ser Phe Glu Asp
155 160 165
Arg Val Ala Lys Ile Val Glu Trp Phe Thr Ser Lys Glu Pro Ile
170 175 180
Asn Leu Gly Leu Leu Tyr Trp Glu Asp Pro Asp Asp Met Gly His
185 190 195
His Leu Gly Pro Asp Ser Pro Leu Met Gly Pro Val Ile Ser Asp
200 205 210
Ile Asp Lys Lys Leu Gly Tyr Leu Ile Gln Met Leu Lys Lys Ala
215 220 225
Lys Leu Trp Asn Thr Leu Asn Leu Ile Ile Thr Ser Asp His Gly
230 235 240
Met Thr Gln Cys Ser Glu Glu Arg Leu Ile Glu Leu Asp Gln Tyr
245 250 255
Leu Asp Lys Asp His Tyr Thr Leu Ile Asp Gln Ser Pro Val Ala
260 265 270
Ala Ile Leu Pro Lys Glu Gly Lys Phe Asp Glu Val Tyr Glu Ala
275 280 285
Leu Thr His Ala His Pro Asn Leu Thr Val Tyr Lys Lys Glu Asp

290	295	300
Val Pro Glu Arg Trp His Tyr Lys Tyr Asn Ser Arg Ile Gln Pro		
305	310	315
Ile Ile Ala Val Ala Asp Glu Gly Trp His Ile Leu Gln Asn Lys		
320	325	330
Ser Asp Asp Phe Leu Leu Gly Asn His Gly Tyr Asp Asn Ala Leu		
335	340	345
Ala Asp Met His Pro Ile Phe Leu Ala His Gly Pro Ala Phe Arg		
350	355	360
Lys Asn Phe Ser Lys Glu Ala Met Asn Ser Thr Asp Leu Tyr Pro		
365	370	375
Leu Leu Cys His Leu Leu Asn Ile Thr Ala Met Pro His Asn Gly		
380	385	390
Ser Phe Trp Asn Val Gln Asp Leu Leu Asn Ser Ala Met Pro Arg		
395	400	405
Val Val Pro Tyr Thr Gln Ser Thr Ile Leu Leu Pro Gly Ser Val		
410	415	420
Lys Pro Ala Glu Tyr Asp Gln Glu Gly Ser Tyr Pro Tyr Phe Ile		
425	430	435
Gly Val Ser Leu Gly Ser Ile Ile Val Ile Val Phe Phe Val Ile		
440	445	450
Phe Ile Lys His Leu Ile His Ser Gln Ile Pro Ala Leu Gln Asp		
455	460	465
Met His Ala Glu Ile Ala Gln Pro Leu Leu Gln Ala		
470	475	

<210> 286

<211> 1337

<212> DNA

<213> Homo sapiens

<400> 286

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tcacacagcc aaaggaggca gagccagac tcacaaccag atccagaggc 200
aacaggacca tggccacctg ggacgaaaag gcagtccacc gcaggggccaa 250
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<210> 287
<211> 255
<212> PRT
<213> Homo sapiens

<400> 287
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Ala Pro Ala Glu Arg Met Ser Lys Phe Leu Arg His Phe Thr Val
20 25 30
Val Gly Asp Asp Tyr His Ala Trp Asn Ile Asn Tyr Lys Lys Trp
35 40 45
Glu Asn Glu Glu Glu Glu Glu Glu Gln Pro Pro Pro Thr
50 55 60
Pro Val Ser Gly Glu Glu Gly Arg Ala Ala Ala Pro Asp Val Ala
65 70 75
Pro Ala Pro Gly Pro Ala Pro Arg Ala Pro Leu Asp Phe Arg Gly
80 85 90
Met Leu Arg Lys Leu Phe Ser Ser His Arg Phe Gln Val Ile Ile
95 100 105
Ile Cys Leu Val Val Leu Asp Ala Leu Leu Val Leu Ala Glu Leu
110 115 120

Ile Leu Asp Leu Lys Ile Ile Gln Pro Asp Lys Asn Asn Tyr Ala
125 130 135
Ala Met Val Phe His Tyr Met Ser Ile Thr Ile Leu Val Phe Phe
140 145 150
Met Met Glu Ile Ile Phe Lys Leu Phe Val Phe Arg Leu Ser Ser
155 160 165
Phe Thr Thr Ser Leu Arg Ser Trp Met Pro Val Val Val Val
170 175 180
Ser Phe Ile Leu Asp Ile Val Leu Leu Phe Gln Glu His Gln Phe
185 190 195
Glu Ala Leu Gly Leu Leu Ile Leu Leu Arg Leu Trp Arg Val Ala
200 205 210
Arg Ile Ile Asn Gly Ile Ile Ile Ser Val Lys Thr Arg Ser Glu
215 220 225
Arg Gln Leu Leu Arg Leu Lys Gln Met Asn Val Gln Leu Ala Ala
230 235 240
Lys Ile Gln His Leu Glu Phe Ser Cys Ser Glu Lys Pro Leu Asp
245 250 255

<210> 288
<211> 3334
<212> DNA
<213> Homo sapiens

<400> 288
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cccagacgca gttccatgtac ttgtgggtca aggggctccc tgccgagctg 150
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<210> 289
<211> 469
<212> PRT
<213> *Homo sapiens*

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<400> 289
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Thr Glu Phe Gln Tyr Phe Glu Ser Lys Gly Leu Pro Ala Glu Leu
      20          25          30
Lys Ser Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe
      35          40          45
Ser Thr Tyr Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp
      50          55          60
Lys Asp Leu Asp Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr
      65          70          75
Leu Gln Asp His Glu Lys Lys Leu Arg Leu Val Phe Lys Ile Leu
      80          85          90

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Ser	Leu	Arg	Asp	Leu	Gly	Val	Lys	Ile	Ser	Glu	Gln	Gln	Ala	Glu
					110					115				120
Lys	Ile	Leu	Lys	Ser	Met	Asp	Lys	Asn	Gly	Thr	Met	Thr	Ile	Asp
					125					130				135
Trp	Asn	Glu	Trp	Arg	Asp	Tyr	His	Leu	Leu	His	Pro	Val	Glu	Asn
					140					145				150
Ile	Pro	Glu	Ile	Ile	Leu	Tyr	Trp	Lys	His	Ser	Thr	Ile	Phe	Asp
					155					160				165
Val	Gly	Glu	Asn	Leu	Thr	Val	Pro	Asp	Glu	Phe	Thr	Val	Glu	Glu
					170					175				180
Arg	Gln	Thr	Gly	Met	Trp	Trp	Arg	His	Leu	Val	Ala	Gly	Gly	Gly
					185					190				195
Ala	Gly	Ala	Val	Ser	Arg	Thr	Cys	Thr	Ala	Pro	Leu	Asp	Arg	Leu
					200					205				210
Lys	Val	Leu	Met	Gln	Val	His	Ala	Ser	Arg	Ser	Asn	Asn	Met	Gly
					215					220				225
Ile	Val	Gly	Gly	Phe	Thr	Gln	Met	Ile	Arg	Glu	Gly	Gly	Ala	Arg
					230					235				240
Ser	Leu	Trp	Arg	Gly	Asn	Gly	Ile	Asn	Val	Leu	Lys	Ile	Ala	Pro
					245					250				255
Glu	Ser	Ala	Ile	Lys	Phe	Met	Ala	Tyr	Glu	Gln	Ile	Lys	Arg	Leu
					260					265				270
Val	Gly	Ser	Asp	Gln	Glu	Thr	Leu	Arg	Ile	His	Glu	Arg	Leu	Val
					275					280				285
Ala	Gly	Ser	Leu	Ala	Gly	Ala	Ile	Ala	Gln	Ser	Ser	Ile	Tyr	Pro
					290					295				300
Met	Glu	Val	Leu	Lys	Thr	Arg	Met	Ala	Leu	Arg	Lys	Thr	Gly	Gln
					305					310				315
Tyr	Ser	Gly	Met	Leu	Asp	Cys	Ala	Arg	Arg	Ile	Leu	Ala	Arg	Glu
					320					325				330
Gly	Val	Ala	Ala	Phe	Tyr	Lys	Gly	Tyr	Val	Pro	Asn	Met	Leu	Gly
					335					340				345
Ile	Ile	Pro	Tyr	Ala	Gly	Ile	Asp	Leu	Ala	Val	Tyr	Glu	Thr	Leu
					350					355				360
Lys	Asn	Ala	Trp	Leu	Gln	His	Tyr	Ala	Val	Asn	Ser	Ala	Asp	Pro
					365					370				375
Gly	Val	Phe	Val	Leu	Leu	Ala	Cys	Gly	Thr	Met	Ser	Ser	Thr	Cys
					380					385				390
Gly	Gln	Leu	Ala	Ser	Tyr	Pro	Leu	Ala	Leu	Val	Arg	Thr	Arg	Met
					395					400				405

Gln Ala Gln Ala Ser Ile Glu Gly Ala Pro Glu Val Thr Met Ser
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Ser Leu Phe Lys His Ile Leu Arg Thr Glu Gly Ala Phe Gly Leu
425 430 435
Tyr Arg Gly Leu Ala Pro Asn Phe Met Lys Val Ile Pro Ala Val
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Ser Ile Ser Tyr Val Val Tyr Glu Asn Leu Lys Ile Thr Leu Gly
455 460 465
Val Gln Ser Arg

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<211> 1658
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<213> Homo sapiens

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<211> 282

<212> PRT

<213> Homo sapiens

<400> 291

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Asp	Ile	Lys	Leu	Ser	Asp	Ile	Val	Ile	Gln	Trp	Leu	Lys	Glu	
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Val	Leu	Gly	Leu	Val	His	Glu	Phe	Lys	Glu	Gly	Lys	Asp	Glu	Leu
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Ser	Glu	Gln	Asp	Glu	Met	Phe	Arg	Gly	Arg	Thr	Ala	Val	Phe	Ala
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Asp	Gln	Val	Ile	Val	Gly	Asn	Ala	Ser	Leu	Arg	Leu	Lys	Asn	Val
	110							115						120
Gln	Leu	Thr	Asp	Ala	Gly	Thr	Tyr	Lys	Cys	Tyr	Ile	Ile	Thr	Ser
	125							130						135
Lys	Gly	Lys	Gly	Asn	Ala	Asn	Leu	Glu	Tyr	Lys	Thr	Gly	Ala	Phe
	140							145						150
Ser	Met	Pro	Glu	Val	Asn	Val	Asp	Tyr	Asn	Ala	Ser	Ser	Glu	Thr

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185	190	195
Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met Lys		Val
200	205	210
Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser		Cys
215	220	225
Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys		Val
230	235	240
Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu		Asn
245	250	255
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 35 40 45
 Gln Glu Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu Met Pro
 50 55 60
 Phe Leu Leu Asn Gln Cys Gly Ser Leu Leu Tyr Tyr Leu Thr Leu
 65 70 75
 Ala Ser Thr Asp Leu Thr Leu Ala Val Pro Ile Cys Asn Ser Leu
 80 85 90
 Ala Ile Ile Phe Thr Leu Ile Val Gly Lys Ala Leu Gly Glu Asp
 95 100 105
 Ile Gly Gly Lys Arg Lys Leu Asp Tyr Cys Glu Cys Gly Thr Gln
 110 115 120
 Leu Cys Gly Ser Arg His Thr Cys Val Ser Ser Phe Pro Glu Pro
 125 130 135
 Ile Ser Pro Glu Trp Val Arg Thr Arg Pro Phe Pro Ile Leu Pro
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Phe Pro Leu Gln Leu Phe Cys Phe Leu Val Ala Ile Arg Val Pro
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Phe Pro Trp Thr Val Trp Arg Lys Thr Glu Ala Gly Val Trp Asp
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<210> 294

<211> 1164

<212> DNA

<213> Homo sapiens

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cggcctaaga tgccacttct tctcatgtcc caggcttgag gcccgtgtt 200

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<212> PRT

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		20							25					30
Ser	Cys	Val	Asn	Ser	Ile	Ala	Ser	Glu	Cys	Pro	Ser	His	Ala	Asn
		35						40						45
Thr	Ser	Cys	Ile	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Leu	Glu	Thr	Pro
		50						55						60
Val	Arg	Leu	Tyr	Gln	Asn	Met	Phe	Cys	Ser	Ala	Glu	Asn	Cys	Ser
		65						70						75
Glu	Glu	Thr	His	Ile	Thr	Ala	Phe	Thr	Val	His	Val	Ser	Ala	Glu
		80						85						90
Glu	His	Phe	His	Phe	Val	Ser	Gln	Cys	Cys	Gln	Gly	Lys	Glu	Cys
		95						100						105
Ser	Asn	Thr	Ser	Asp	Ala	Leu	Asp	Pro	Pro	Leu	Lys	Asn	Val	Ser
		110						115						120
Ser	Asn	Ala	Glu	Cys	Pro	Ala	Cys	Tyr	Glu	Ser	Asn	Gly	Thr	Ser
		125						130						135
Cys	Arg	Gly	Lys	Pro	Trp	Lys	Cys	Tyr	Glu	Glu	Glu	Gln	Cys	Val
		140						145						150
Phe	Leu	Val	Ala	Glu	Leu	Lys	Asn	Asp	Ile	Glu	Ser	Lys	Ser	Leu
		155						160						165
Val	Leu	Lys	Gly	Cys	Ser	Asn	Val	Ser	Asn	Ala	Thr	Cys	Gln	Phe
		170						175						180
Leu	Ser	Gly	Glu	Asn	Lys	Thr	Leu	Gly	Gly	Val	Ile	Phe	Arg	Lys
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Phe	Glu	Cys	Ala	Asn	Val	Asn	Ser	Leu	Thr	Pro	Thr	Ser	Ala	Pro
		200							205					210
Thr	Thr	Ser	His	Asn	Val	Gly	Ser	Lys	Ala	Ser	Leu	Tyr	Leu	Leu
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<212> DNA

<213> Homo sapiens

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<211> 341

<212> PRIM

<213> Homo sapiens

<400> 297

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														30
20								25						

Thr	Glu	Met	Gln	Arg	Val	Ser	Leu	Arg	Phe	Gly	Gly	Pro	Met	Thr
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35								40						

Arg	Ser	Tyr	Arg	Ser	Thr	Ala	Arg	Thr	Gly	Leu	Pro	Arg	Lys	Thr
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50								55						

Arg	Ile	Ile	Leu	Glu	Asp	Glu	Asn	Asp	Ala	Met	Ala	Asp	Ala	Asp
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95	100	105
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110	115	120
Ser Arg Glu Leu Pro Ser Ala Thr Pro	Asn Thr Ala Gly Ser Ser	
125	130	135
Ser Thr Arg Phe Ile Ala Asn Ser Gln	Glu Pro Glu Ile Arg Leu	
140	145	150
Thr Ser Ser Leu Pro Arg Ser Pro Gly Arg Ser Thr Glu Asp Leu		
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Pro Gly Ser Gln Ala Thr Leu Ser Gln Trp Ser Thr Pro Gly Ser		
170	175	180
Thr Pro Ser Arg Trp Pro Ser Pro Ser Pro Thr Ala Met Pro Ser		
185	190	195
Pro Glu Asp Leu Arg Leu Val Leu Met Pro Trp Gly Pro Trp His		
200	205	210
Cys His Cys Lys Ser Gly Thr Met Ser Arg Ser Arg Ser Gly Lys		
215	220	225
Leu His Gly Leu Ser Gly Arg Leu Arg Val Gly Ala Leu Ser Gln		
230	235	240
Leu Arg Thr Glu His Lys Pro Cys Thr Tyr Gln Gln Cys Pro Cys		
245	250	255
Asn Arg Leu Arg Glu Glu Cys Pro Leu Asp Thr Ser Leu Cys Thr		
260	265	270
Asp Thr Asn Cys Ala Ser Gln Ser Thr Thr Ser Thr Arg Thr Thr		
275	280	285
Thr Thr Pro Phe Pro Thr Ile His Leu Arg Ser Ser Pro Ser Leu		
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 35 40 45
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 50 55 60
 Gly Trp Thr Cys Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val
 65 70 75

Thr Val Gly Leu Tyr Leu Gln Glu Gly His Lys Val Pro Gln Phe
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 His Gly Lys Trp Pro Phe Ser Arg Phe Leu Phe Phe Gln Glu Pro
 95 105
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 110 115 120
 Met Leu Cys Arg Tyr Arg Thr Phe Val Pro Ala Ser Ser Pro Met
 125 130 135
 Tyr His Thr Cys Val Ala Phe Ala Trp Val Ser Leu Asn Ala Trp
 140 145 150
 Phe Trp Ser Thr Val Phe His Thr Arg Asp Thr Asp Leu Thr Glu
 155 160 165
 Lys Met Asp Tyr Phe Cys Ala Ser Thr Val Ile Leu His Ser Ile
 170 175 180
 Tyr Leu Cys Cys Val Arg Thr Val Gly Leu Gln His Pro Ala Val
 185 190 195
 Val Ser Ala Phe Arg Ala Leu Leu Leu Met Leu Thr Val His
 200 205 210
 Val Ser Tyr Leu Ser Leu Ile Arg Phe Asp Tyr Gly Tyr Asn Leu
 215 220 225
 Val Ala Asn Val Ala Ile Gly Leu Val Asn Val Val Trp Trp Leu
 230 235 240
 Ala Trp Cys Leu Trp Asn Gln Arg Arg Leu Pro His Val Arg Lys
 245 250 255
 Cys Val Val Val Leu Leu Leu Gln Gly Leu Ser Leu Leu Glu
 260 265 270
 Leu Leu Asp Phe Pro Pro Leu Phe Trp Val Leu Asp Ala His Ala
 275 280 285
 Ile Trp His Ile Ser Thr Ile Pro Val His Val Leu Phe Phe Ser
 290 295 300
 Phe Leu Glu Asp Asp Ser Leu Tyr Leu Leu Lys Glu Ser Glu Asp
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 Lys Phe Lys Leu Asp
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<210> 300

<211> 1674

<212> DNA

<213> Homo sapiens

<400> 300

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gcagcaccaa agaaacggag agaaaagaaa ccaaagccga ggaggagctg 250
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<210> 301

<211> 461
<212> PRT
<213> Homo sapiens

<400> 301
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35 40 45
Ser Ser Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu
50 55 60
Glu Leu Asp Ala Glu Val Leu Glu Val Phe His Pro Thr His Glu
65 70 75
Trp Gln Ala Leu Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His
80 85 90
Val Arg Leu Asn Leu Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln
95 100 105
Tyr Glu Asp Lys Phe Arg Asn Asn Leu Lys Gly Lys Arg Leu Asp
110 115 120
Ile Asn Thr Asn Thr Tyr Thr Ser Gln Asp Leu Lys Ser Ala Leu
125 130 135
Ala Lys Phe Lys Glu Gly Ala Glu Met Glu Ser Ser Lys Glu Asp
140 145 150
Lys Ala Arg Gln Ala Glu Val Lys Arg Leu Phe Arg Pro Ile Glu
155 160 165
Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val Val Ile Glu Thr
170 175 180
Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe Asn Ser Ser
185 190 195
Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp Leu Glu
200 205 210
Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser Phe
215 220 225
Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro
230 235 240
Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser
245 250 255
Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Ala Leu
260 265 270
Gln Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala
275 280 285
Lys Lys Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe

290	295	300
Pro Tyr Ala Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val		
305	310	315
Leu Arg Thr Leu Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val		
320	325	330
Arg Val Val Thr Leu Leu Tyr Asp Leu Val Thr Glu Lys Met Phe		
335	340	345
Ala Glu Glu Ala Glu Leu Thr Gln Glu Met Ser Pro Glu Lys		
350	355	360
Leu Gln Gln Tyr Arg Gln Val His Leu Leu Pro Gly Leu Trp Glu		
365	370	375
Gln Gly Trp Cys Glu Ile Thr Ala His Leu Leu Ala Leu Pro Glu		
380	385	390
His Asp Ala Arg Glu Lys Val Leu Gln Thr Leu Gly Val Leu Leu		
395	400	405
Thr Thr Cys Arg Asp Arg Tyr Arg Gln Asp Pro Gln Leu Gly Arg		
410	415	420
Thr Leu Ala Ser Leu Gln Ala Glu Tyr Gln Val Leu Ala Ser Leu		
425	430	435
Glu Leu Gln Asp Gly Glu Asp Glu Gly Tyr Phe Gln Glu Leu Leu		
440	445	450
Gly Ser Val Asn Ser Leu Leu Lys Glu Leu Arg		
455	460	

<210> 302

<211> 2136

<212> DNA

<213> Homo sapiens

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tcccatttgc ctgtcttggt caggccccca ccccccattcc cacctgacca 200
gccccatggggc ctgcgggtgt tttcggctgc actttcgctc cggttcggccc 250
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gggttagcat cgctgagtga ggacggaaga tcacccatct ccatccggcca 550

卷之三

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gtgagctggc cactcccgag ctgcagtgcctt actggaggag tcagactacc 1900
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ttgtggggagg gccccccgggt tttctataaa ctgtatcatt ttctgctgag 2000
gggtggagggtt cccatccctttaatcaaggat gattgtgatt ttgactaata 2050
aaaaagaatt tgaa 2100
aaaaaaaaaaaaa aaaaaaaaaaaaaa aaaaaaaaaaaaaa aaaaaaaaaa 2136

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<210> 303
<211> 247
<212> PRT
<213> Homo sapiens

<400> 303
Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly
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Arg Val Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser
35 40 45
Leu Leu Leu Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr
50 55 60
Asp Arg Ser Asp Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly
65 70 75
Ala Ala Val Ser Val Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr
80 85 90
Tyr Lys Leu Leu Lys Lys Ala Asp Glu Gly Leu Ala Ser Leu Ser
95 100 105
Glu Asp Gly Arg Ser Pro Ile Ser Ile Arg Gln Met Ala Tyr Val
110 115 120
Ser Gly Leu Ser Phe Gly Ile Ile Ser Gly Val Phe Ser Val Ile
125 130 135
Asn Ile Leu Ala Asp Ala Leu Gly Pro Gly Val Val Gly Ile His
140 145 150
Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser Ala Phe Leu Thr Ala
155 160 165
Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val Val Phe Phe Asp
170 175 180
Ala Cys Glu Arg Arg Tyr Trp Ala Leu Gly Leu Val Val Gly
185 190 195
Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro Trp Tyr
200 205 210
Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met Gly
215 220 225
Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln
230 235 240
Arg Ser Leu Leu Cys Lys Asp
245

<210> 304
<211> 240
<212> DNA
<213> Homo sapiens

<220>

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<221> unsure
<222> 108, 123, 126, 154, 198, 206, 217
<223> unknown base

<400> 304
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ccttcggnat catcagtgtt gtnttntctg ttatcaatat tttggctgat 150
gcantgggc caggtgtgtt tgggatccat ggagactcac cctattattt 200
cctganttca gccttntga cagcagccat tatcctgctc 240

<210> 305
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 58, 94, 132, 186, 191, 220, 240, 248, 280, 311, 332
<223> unknown base

<400> 305
gaccgaccgt tcagatgccg gttccagta cggttcctg attttggtg 50
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ctgcttaaga aggcagatga ggggttagca tngctgatgtt aggacggaag 150
atcacccatt tccatccgcg agatggccta tgtttntgtt ntcccttcg 200
gtatcatcaag tggtgtttt tctgttatca atattttggm tgatgcantt 250
ggccaggtt tggttggat ccatggagan tcaccctatt aattcctgaa 300
ttcagccctt ntgacagcag ccattatcct gntccatacc ttttggggag 350
ttgtgtttt tgatgcctgt gagaggag 378

<210> 306
<211> 655
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1, 22, 129, 133, 184
<223> unknown base

<400> 306
ngttggagaa gtggcgcgga ctttcatttgggtttcggt ttccccccctt 50
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gcgttgccac cccacgcggaa ctccccagt ggngegcctt tcccatgtc 150
ctgtctgtt caggccccca ccccccatttcc cacntgacca gccatgggg 200
ctgcgggtt ttccggctgc actttcgctc cgttcgcccc ggcccttcgcg 250

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cgcaggggca tttttcttgc tggtctccct gctcctggcc tctgtggct 350
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gtttctggtc tctccttccg tatcatcagt ggtgtctct ctgttatcaa 600
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caccc 655

<210> 307
<211> 650
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 52, 89, 128
<223> unknown base

<400> 307
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cgttgccacc ccacgcggac tccccagntg ggcgcnnncc cccatttgc 150
tgtcttggtc agggcccccac cccccttccc acctgaccag ccatgggggc 200
tgcgggtttt ttccggctgc actttctgc cggtcgccg cggcccttcgc 250
gcttttcttg atcaactgtgg ctggggaccg gcttcggcggtt atcatcttgg 300
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tgggtcatct tggccatgtt gacccggccg tcagatgccc ggtcccgatg 400
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tcgctgagtgg aggccggaa atcacccatc tccatccggcc agatggccta 550
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<210> 308
<211> 1570
<212> DNA
<213> Homo sapiens

<400> 308
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gctgggagca aatccccac cccctacctg ggggacaggg caagtggagac 150
ctggtgaggg tggctcagca ggcaggaaag gagaggtgtc tgtgcgtct 200
gcacccacat ctttcctgt cccctccttgc ccctgtctgg aggctgctag 250
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ccgtctcggc cactactccc tgcaccatgt ttatgtatct gggcagcaga 750
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cactctaactg acctcatgtc catcaaactg aacagaagaa ttccgtccac 850
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ctgagaagtg gaaaaaaaaa 1550

<210> 309

<211> 293
<212> PRT
<213> Homo sapiens

<400> 309
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20 25 30
Asn Asp Val Ser Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly
35 40 45
Ser Asn Gln Asp Leu Gly Ala Gly Glu Asp Ala Arg Ser
50 55 60
Asp Asp Ser Ser Arg Ile Ile Asn Gly Ser Asp Cys Asp Met
65 70 75
His Thr Gln Pro Trp Gln Ala Ala Leu Leu Arg Pro Asn Gln
80 85 90
Leu Tyr Cys Gly Ala Val Leu Val His Pro Gln Trp Leu Leu Thr
95 100 105
Ala Ala His Cys Arg Lys Lys Val Phe Arg Val Arg Leu Gly His
110 115 120
Tyr Ser Leu Ser Pro Val Tyr Glu Ser Gly Gln Gln Met Phe Gln
125 130 135
Gly Val Lys Ser Ile Pro His Pro Gly Tyr Ser His Pro Gly His
140 145 150
Ser Asn Asp Leu Met Leu Ile Lys Leu Asn Arg Arg Ile Arg Pro
155 160 165
Thr Lys Asp Val Arg Pro Ile Asn Val Ser Ser His Cys Pro Ser
170 175 180
Ala Gly Thr Lys Cys Leu Val Ser Gly Trp Gly Thr Thr Lys Ser
185 190 195
Pro Gln Val His Phe Pro Lys Val Leu Gln Cys Leu Asn Ile Ser
200 205 210
Val Leu Ser Gln Lys Arg Cys Glu Asp Ala Tyr Pro Arg Gln Ile
215 220 225
Asp Asp Thr Met Phe Cys Ala Gly Asp Lys Ala Gly Arg Asp Ser
230 235 240
Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly Ser Leu
245 250 255
Gln Gly Leu Val Ser Trp Gly Asp Tyr Pro Cys Ala Arg Pro Asn
260 265 270
Arg Pro Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Lys Trp Ile
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Gln Glu Thr Ile Gln Ala Asn Ser

TIGRITY:19587660

<210> 310
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 310
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<210> 311
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 311
ctggaacatc tgctgccag attc 24

<210> 312
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
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<210> 313
<211> 3010
<212> DNA
<213> Homo sapiens

<400> 313
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ccgtgtgtgt ggccctggct gtgtgtgtgg ctgtagttgtt caccgggtcc 150
gtgtctttcc tgaaccacgc ccacgcgcgc ggcacggcgc ccccacctgt 200
cgtcagcact ggggtgcaca ggcacaaacg cgccctggtc actgtggaaa 250
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<210> 314
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<212> PRT
<213> *Homo sapiens*

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Glu Asp Arg Pro Arg Asp Lys Pro Gln Arg Pro Ser Cys Gly Tyr
      20          25          30
Val Leu Cys Thr Val Leu Leu Ala Leu Ala Val Leu Leu Ala Val
      35          40          45
Ala Val Thr Gly Ala Val Leu Phe Leu Asn His His Ala His Ala Pro
      50          55          60
Gly Thr Ala Pro Pro Pro Val Val Ser Thr Gly Ala Ala Ser Ala
      65          70          75
Asn Ser Ala Leu Val Thr Val Glu Arg Ala Asp Ser Ser His Leu
      80          85          90
Ser Ile Leu Ile Asp Pro Arg Cys Pro Asp Leu Thr Asp Ser Phe
      95          100         105

```

TENETESESTEST

Ala Arg Leu Glu Ser Ala Gln Ala Ser Val Leu Gln Ala Leu Thr
110 115 120
Glu His Gln Ala Gln Pro Arg Leu Val Gly Asp Gln Glu Gln Glu
125 130 135
Leu Leu Asp Thr Leu Ala Asp Gln Leu Pro Arg Leu Leu Ala Arg
140 145 150
Ala Ser Glu Leu Gln Thr Glu Cys Met Gly Leu Arg Lys Gly His
155 160 165
Gly Thr Leu Gly Gln Gly Leu Ser Ala Leu Gln Ser Glu Gln Gly
170 175 180
Arg Leu Ile Gln Leu Leu Ser Glu Ser Gln Gly His Met Ala His
185 190 195
Leu Val Asn Ser Val Ser Asp Ile Leu Asp Ala Leu Gln Arg Asp
200 205 210
Arg Gly Leu Gly Arg Pro Arg Asn Lys Ala Asp Leu Gln Arg Ala
215 220 225
Pro Ala Arg Gly Thr Arg Pro Arg Gly Cys Ala Thr Gly Ser Arg
230 235 240
Pro Arg Asp Cys Leu Asp Val Leu Leu Ser Gly Gln Gln Asp Asp
245 250 255
Gly Val Tyr Ser Val Phe Pro Thr His Tyr Pro Ala Gly Phe Gln
260 265 270
Val Tyr Cys Asp Met Arg Thr Asp Gly Gly Gly Trp Thr Val Phe
275 280 285
Gln Arg Arg Glu Asp Gly Ser Val Asn Phe Phe Arg Gly Trp Asp
290 295 300
Ala Tyr Arg Asp Gly Phe Gly Arg Leu Thr Gly Glu His Trp Leu
305 310 315
Gly Leu Lys Arg Ile His Ala Leu Thr Thr Gln Ala Ala Tyr Glu
320 325 330
Leu His Val Asp Leu Glu Asp Phe Glu Asn Gly Thr Ala Tyr Ala
335 340 345
Arg Tyr Gly Ser Phe Gly Val Gly Leu Phe Ser Val Asp Pro Glu
350 355 360
Glu Asp Gly Tyr Pro Leu Thr Val Ala Asp Tyr Ser Gly Thr Ala
365 370 375
Gly Asp Ser Leu Leu Lys His Ser Gly Met Arg Phe Thr Thr Lys
380 385 390
Asp Arg Asp Ser Asp His Ser Glu Asn Asn Cys Ala Ala Phe Tyr
395 400 405
Arg Gly Ala Trp Trp Tyr Arg Asn Cys His Thr Ser Asn Leu Asn
410 415 420

Gly Gln Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala Asp Gly Val
425 430 435

Glu Trp Ser Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys Phe Ser
440 445 450

Glu Met Lys Ile Arg Pro Val Arg Glu Asp Arg
455 460

<210> 315
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 315
cacacgtcca acctcaatgg gcag 24

<210> 316
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 316
gaccagcagg gccaaggaca agg 23

<210> 317
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 317
gttctctgag atgaagatcc ggccggccg ggagtaccgc ttag 44

<210> 318
<211> 1841
<212> DNA
<213> Homo sapiens

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ccaagtacag cagcacgagg gacatgtgg atgatgtgg ggacaccacc 200
atgagcctgc attctcaagc ctctggccaca actcggcatc cagagccccg 250
gcccacacag cacagggttc cctttcaac gtggcgacca gtggccctga 300
ccctgtgtac ttgtgtcttgc gtgtgtgtga tagggctggc agccctgggg 350
cttttgtttt ttcagttacta ccagtcgtcc aatactggtc aagacaccat 400

ESTATE 60

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tgtggccatc ctcataatggaa tgatcttc aaaggactgc aaagaattga 900
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<210> 319
<211> 280
<212> PRT
<213> Homo sapiens

<400> 319
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Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr
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35 40 45
Thr Trp Arg Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val
50 55 60
Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr
65 70 75
Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu
80 85 90
Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser Leu Gln Val
95 100 105
Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala Glu Lys
110 115 120
Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser
125 130 135
Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln
140 145 150
Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys
155 160 165
Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp
170 175 180
Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser
185 190 195
Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu
200 205 210
Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile
215 220 225
Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu
230 235 240
Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys
245 250 255
Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His
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Val Pro Pro Glu Thr Leu Gly Glu Gly Asp
275 280

<210> 320
<211> 468
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 59, 95, 149, 331, 364, 438, 446
<223> unknown base

<400> 320
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ccttttcaa cgtggcgacc agtggccctg accctgctga ctgtgtctt 200
ggtgctgctg atagggtgg cagccctggg gctttgttt tttcagta 250
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gcttgcaggag agtnlgcagc atgtggctga aaaactctgt cgtgagctgt 400
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<210> 321
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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atgcaggccca agtacagcagc cac 23

<210> 322
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<400> 322
catgctgacg acttcctgca agc 23

<210> 323
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 323
ccacacagtc tctgtttttt ggg 23

<210> 324
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
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atgtctggatg atgatgggga caccaccatg agcctgcatt 40

<210> 325
<211> 2988
<212> DNA
<213> Homo sapiens

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DRAFT

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gccccccagag ctggccgtg acactggccg ctttgc tgc c a g g c a 2250
g c g a g g c c t g c t t c a c a a c t c g a c t a c g t g g c c t g 2300
g c g c a g c c t c a g a a a g a g g a g c t g c t g a g g c c 2350
c g a g c t g t c t c t c a c t t c t c a g t c t g c a t g c g g g a g c 2400
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c c g a a c c c a g t g c t c a c t t t g a a c a g g a g c a g g a c a 2550
c c t g a c c c c a c c t t t c c c g t g c t c c c g c a c c c a c c c 2600
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g c c g t a g c c a g c c a a c a g t g c c a c t g t g c t c t c t g 2700
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g c t g t g g c c t c a c g t a t t t a t g c a g t a c a g t c t g a c c c a c c c 2850
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gctccctgcc ttaataaac tggccaagtg tggaaaaa 2988

<210> 326

<211> 775

<212> PRT

<213> Homo sapiens

<400> 326

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20 25 30

Val Thr Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro
35 40 45

Gly Asp Ser Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg
50 55 60

Arg Pro Asn Ser Val Gln Pro Gly Ala Glu Arg Glu Lys Pro Gly
65 70 75

Ala Gly Glu Gly Ala Gly Glu Asn Trp Glu Pro Arg Val Leu Pro
80 85 90

Tyr His Pro Ala Gln Pro Gly Gln Ala Ala Lys Lys Ala Val Arg
95 100 105

Thr Arg Tyr Ile Ser Thr Glu Leu Gly Ile Arg Gln Arg Leu Leu
110 115 120

Val Ala Val Leu Thr Ser Gln Thr Thr Leu Pro Thr Leu Gly Val
125 130 135

Ala Val Asn Arg Thr Leu Gly His Arg Leu Glu Arg Val Val Phe
140 145 150

Leu Thr Gly Ala Arg Gly Arg Arg Ala Pro Pro Gly Met Ala Val
155 160 165

Val Thr Leu Gly Glu Glu Arg Pro Ile Gly His Leu His Leu Ala
170 175 180

Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe Asp Trp Phe
185 190 195

Phe Leu Val Pro Asp Thr Thr Tyr Thr Glu Ala His Gly Leu Ala
200 205 210

Arg Leu Thr Gly His Leu Ser Leu Ala Ser Ala Ala His Leu Tyr
215 220 225

Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Glu Pro Thr Pro Gly
230 235 240

Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Met Leu
245 250 255

Leu Gln Gln Leu Arg Pro His Leu Glu Gly Cys Arg Asn Asp Ile
260 265 270

Val Ser Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp
 275 280 285
 Ala Thr Gly Val Gly Cys Thr Gly Asp His Glu Gly Val His Tyr
 290 295 300
 Ser His Leu Glu Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp
 305 310 315
 Pro His Phe Arg Ser Ala Leu Thr Ala His Pro Val Arg Asp Pro
 320 325 330
 Val His Met Tyr Gln Leu His Lys Ala Phe Ala Arg Ala Glu Leu
 335 340 345
 Glu Arg Thr Tyr Gln Glu Ile Gln Glu Leu Gln Trp Glu Ile Gln
 350 355 360
 Asn Thr Ser His Leu Ala Val Asp Gly Asp Arg Ala Ala Ala Trp
 365 370 375
 Pro Val Gly Ile Pro Ala Pro Ser Arg Pro Ala Ser Arg Phe Glu
 380 385 390
 Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln His Ala Phe Ser Cys
 395 400 405
 Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly Ala Asp Arg Ala
 410 415 420
 Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu Leu Asn Arg
 425 430 435
 Arg Tyr His Pro Ala Leu Arg Leu Gln Lys Gln Gln Leu Val Asn
 440 445 450
 Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu
 455 460 465
 Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Arg Pro
 470 475 480
 Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu
 485 490 495
 Ile Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val
 500 505 510
 Leu Leu Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Pro Gly Phe
 515 520 525
 Leu Glu Ala Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala
 530 535 540
 Ala Ala Leu Thr Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln
 545 550 555
 Arg Val Ala His Ala Asp Val Phe Ala Pro Val Lys Ala His Val
 560 565 570
 Ala Glu Leu Glu Arg Arg Phe Pro Gly Ala Arg Val Pro Trp Leu
 575 580 585

Ser Val Gln Thr Ala Ala Pro Ser Pro Leu Arg Leu Met Asp Leu
590 595 600
Leu Ser Lys Lys His Pro Leu Asp Thr Leu Phe Leu Leu Ala Gly
605 610 615
Pro Asp Thr Val Leu Thr Pro Asp Phe Leu Asn Arg Cys Arg Met
620 625 630
His Ala Ile Ser Gly Trp Gln Ala Phe Phe Pro Met His Phe Gln
635 640 645
Ala Phe His Pro Gly Val Ala Pro Pro Gln Gly Pro Gly Pro Pro
650 655 660
Glu Leu Gly Arg Asp Thr Gly Arg Phe Asp Arg Gln Ala Ala Ser
665 670 675
Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg Gly Arg
680 685 690
Leu Ala Ala Ala Ser Glu Gln Glu Glu Leu Leu Glu Ser Leu
695 700 705
Asp Val Tyr Glu Leu Phe Leu His Phe Ser Ser Leu His Val Leu
710 715 720
Arg Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Thr
725 730 735
Cys Ser Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Leu Gln
740 745 750
Ser Val Leu Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu
755 760 765
Leu Phe Glu Gln Glu Gln Gly Asn Ser Thr
770 775

<210> 327

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 327

tggaaaggctg ccgcacacgac aatc 24

<210> 328

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 328

ctgtatgtgc cgatgttctg 20

<210> 329

<211> 20

<212> DNA
<213> Artificial Sequence

<220>
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<400> 329
atggctcagt gtgcagacag 20

<210> 330
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<220>
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<400> 330
gcatgctgct ccgtgaagta gtcc 24

<210> 331
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 331
atgcattggaa aagaaggccc gcc 24

<210> 332
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 332
tgcactggtg accacgaggg ggtgcactat agccatctgg agcttag 47

<210> 333
<211> 1095
<212> DNA
<213> Homo sapiens

<400> 333
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gccacgacaa ctggaggcaa agagggttgc tcaacgcccc gcctcattgg 400

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<210> 334

<211> 153

<212> PRT

<213> Homo sapiens

<400> 334

Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg	Leu Ala		
1	5	10	15
Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val	Arg Trp Glu		
20	25	30	
Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala	Val Ala Gly		
35	40	45	
Lys Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp	Pro Glu		
50	55	60	
Pro Glu Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser	His Gly		
65	70	75	
Tyr Asp Lys Asp Pro Val Leu Asp Val Trp Asn Met Arg	Leu Val		
80	85	90	
Phe Phe Phe Gly Val Ser Ile Ile Leu Val Leu Gly Ser	Thr Phe		
95	100	105	
Val Ala Tyr Leu Pro Asp Tyr Arg Met Lys Glu Trp Ser	Arg Arg		
110	115	120	
Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn Gly	Leu Pro		
125	130	135	
Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln	Leu Pro		
140	145	150	

Glu Asp Glu

<210> 335
<211> 442
<212> DNA
<213> Homo sapiens

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gaccacaccg tggcaagagg acccagaacc cgaggacgaa aacttgtatg 200
agaagaaccg agactcccat gtttatgaca aggaccccg tttggacgtc 250
tggAACATGC gacttgtctt ctgtttggc gtctccatca tcctggtc 300
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<210> 336
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 336
ctgagaccct gcagcaccat ctg 23

<210> 337
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 337
ggtgcttc tt gagccccact tagc 24

<210> 338
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 338
aatcttagctt ctccaggact gtggtagccc cgtcccgctgt 40

<210> 339
<211> 2162
<212> DNA

<213> Homo sapiens

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acgcgcgtggg attcggagct tcagcggaa ggagtgtccc attacaggct 200
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ctactttctg cgctatgctg tgctgcgcgc ggaggtggtc tgacccgaaa 550
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<210> 340

<211> 574

<212> PRT

<213> Homo sapiens

<400> 340

Met	Pro	Leu	Ala	Leu	Leu	Val	Leu	Leu	Leu	Gly	Pro	Gly	Gly
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Trp	Cys	Leu	Ala	Glu	Pro	Pro	Arg	Asp	Ser	Leu	Arg	Glu	Glu	Leu
				20					25					30

Val	Ile	Thr	Pro	Leu	Pro	Ser	Gly	Asp	Val	Ala	Ala	Thr	Phe	Gln
						35						40		45

Phe	Arg	Thr	Arg	Trp	Asp	Ser	Glu	Leu	Gln	Arg	Glu	Gly	Val	Ser
				50					55					60

His	Tyr	Arg	Leu	Phe	Pro	Lys	Ala	Leu	Gly	Gln	Leu	Ile	Ser	Lys
				65					70					75

Tyr	Ser	Leu	Arg	Glu	Leu	His	Leu	Ser	Phe	Thr	Gln	Gly	Phe	Trp
				80				85						90

Arg	Thr	Arg	Tyr	Trp	Gly	Pro	Pro	Phe	Leu	Gln	Ala	Pro	Ser	Gly
				95					100					105

Ala	Glu	Leu	Trp	Val	Trp	Phe	Gln	Asp	Thr	Val	Thr	Asp	Val	Asp
				110					115					120

Lys	Ser	Trp	Lys	Glu	Leu	Ser	Asn	Val	Leu	Ser	Gly	Ile	Phe	Cys
				125					130					135

Ala	Ser	Leu	Asn	Phe	Ile	Asp	Ser	Thr	Asn	Thr	Val	Thr	Pro	Thr
				140					145					150

Ala Ser Phe Lys Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr
 155 160 165
 Phe Leu Arg Tyr Ala Val Leu Pro Arg Glu Val Val Cys Thr Glu
 170 175 180
 Asn Leu Thr Pro Trp Lys Lys Leu Leu Pro Cys Ser Ser Lys Ala
 185 190 195
 Gly Leu Ser Val Leu Leu Lys Ala Asp Arg Leu Phe His Thr Ser
 200 205 210
 Tyr His Ser Gln Ala Val His Ile Arg Pro Val Cys Arg Asn Ala
 215 220 225
 Arg Cys Thr Ser Ile Ser Trp Glu Leu Arg Gln Thr Leu Ser Val
 230 235 240
 Val Phe Asp Ala Phe Ile Thr Gly Gln Gly Lys Lys Asp Trp Ser
 245 250 255
 Leu Phe Arg Met Phe Ser Arg Thr Leu Thr Glu Pro Cys Pro Leu
 260 265 270
 Ala Ser Glu Ser Arg Val Tyr Val Asp Ile Thr Thr Tyr Asn Gln
 275 280 285
 Asp Asn Glu Thr Leu Glu Val His Pro Pro Pro Thr Thr Thr Tyr
 290 295 300
 Gln Asp Val Ile Leu Gly Thr Arg Lys Thr Tyr Ala Ile Tyr Asp
 305 310 315
 Leu Leu Asp Thr Ala Met Ile Asn Asn Ser Arg Asn Leu Asn Ile
 320 325 330
 Gln Leu Lys Trp Lys Arg Pro Pro Glu Asn Glu Ala Pro Pro Val
 335 340 345
 Pro Phe Leu His Ala Gln Arg Tyr Val Ser Gly Tyr Gly Leu Gln
 350 355 360
 Lys Gly Glu Leu Ser Thr Leu Leu Tyr Asn Thr His Pro Tyr Arg
 365 370 375
 Ala Phe Pro Val Leu Leu Leu Asp Thr Val Pro Trp Tyr Leu Arg
 380 385 390
 Leu Tyr Val His Thr Leu Thr Ile Thr Ser Lys Gly Lys Glu Asn
 395 400 405
 Lys Pro Ser Tyr Ile His Tyr Gln Pro Ala Gln Asp Arg Leu Gln
 410 415 420
 Pro His Leu Leu Glu Met Leu Ile Gln Leu Pro Ala Asn Ser Val
 425 430 435
 Thr Lys Val Ser Ile Gln Phe Glu Arg Ala Leu Leu Lys Trp Thr
 440 445 450
 Glu Tyr Thr Pro Asp Pro Asn His Gly Phe Tyr Val Ser Pro Ser
 455 460 465

Val Leu Ser Ala Leu Val Pro Ser Met Val Ala Ala Lys Pro Val
470 475 480

Asp Trp Glu Glu Ser Pro Leu Phe Asn Ser Leu Phe Pro Val Ser
485 490 495

Asp Gly Ser Asn Tyr Phe Val Arg Leu Tyr Thr Glu Pro Leu Leu
500 505 510

Val Asn Leu Pro Thr Pro Asp Phe Ser Met Pro Tyr Asn Val Ile
515 520 525

Cys Leu Thr Cys Thr Val Val Ala Val Cys Tyr Gly Ser Phe Tyr
530 535 540

Asn Leu Leu Thr Arg Thr Phe His Ile Glu Glu Pro Arg Thr Gly
545 550 555

Gly Leu Ala Lys Arg Leu Ala Asn Leu Ile Arg Arg Ala Arg Gly
560 565 570

Val Pro Pro Leu

<210> 341

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

tggacacccgt accctggat ctgc 24

<210> 342

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic oligonucleotide probe

<400> 342

ccaactctga ggagagcaag tggc 24

<210> 343

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

tgtatgtgca caccctcacc atcacctcca agggcaaggaa gaac 44

<210> 344

<211> 762

<212> DNA

<213> Homo sapiens

Homo sapiens

<400> 344
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tttataatcc aa 762

<210> 345
<211> 111
<212> PRT
<213> Homo sapiens

<400> 345
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Val Thr Leu Val Ala Val Glu Gly Val Lys Glu Gly Ile Glu Lys
20 25 30
Ala Gly Val Cys Pro Ala Asp Asn Val Arg Cys Phe Lys Ser Asp
35 40 45
Pro Pro Gln Cys His Thr Asp Gln Asp Cys Leu Gly Glu Arg Lys
50 55 60
Cys Cys Tyr Leu His Cys Gly Phe Lys Cys Val Ile Pro Val Lys
65 70 75
Glu Leu Glu Glu Gly Gly Asn Lys Asp Glu Asp Val Ser Arg Pro
80 85 90
Tyr Pro Glu Pro Gly Trp Glu Ala Lys Cys Pro Gly Ser Ser Ser
95 100 105
Thr Arg Cys Pro Gln Lys
110

TATTTCTTGTGCGG

<210> 346
<211> 2528
<212> DNA
<213> Homo sapiens

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<210> 347
<211> 600
<212> PRT
<213> *Homo sapiens*

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<400> 347
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Gln Trp Ser Leu Leu Leu Ala Val Leu Val Phe Phe Leu Phe Ala
      20          25          30

Leu Pro Ser Phe Ile Lys Glu Pro Gln Thr Lys Pro Ser Arg His
      35          40          45

Gln Arg Thr Glu Asn Ile Lys Glu Arg Ser Leu Gln Ser Leu Ala
      50          55          60

Lys Pro Lys Ser Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile

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HOTYKET-HSGT6650

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Tyr Ala Glu Pro Ala Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr 80	85	90
Gln Pro Lys Ala His Thr Thr Gly Asp Arg Gly Lys Glu Ala Asn 95	100	105
Gln Ala Pro Pro Glu Glu Gln Asp Lys Val Pro His Thr Ala Gln 110	115	120
Arg Ala Ala Trp Lys Ser Pro Glu Lys Glu Lys Thr Met Val Asn 125	130	135
Thr Leu Ser Pro Arg Gly Gln Asp Ala Gly Met Ala Ser Gly Arg 140	145	150
Thr Glu Ala Gln Ser Trp Lys Ser Gln Asp Thr Lys Thr Thr Gln 155	160	165
Gly Asn Gly Gly Gln Thr Arg Lys Leu Thr Ala Ser Arg Thr Val 170	175	180
Ser Glu Lys His Gln Gly Lys Ala Ala Thr Thr Ala Lys Thr Leu 185	190	195
Ile Pro Lys Ser Gln His Arg Met Leu Ala Pro Thr Gly Ala Val 200	205	210
Ser Thr Arg Thr Arg Gln Lys Gly Val Thr Thr Ala Val Ile Pro 215	220	225
Pro Lys Glu Lys Lys Pro Gln Ala Thr Pro Pro Pro Ala Pro Phe 230	235	240
Gln Ser Pro Thr Thr Gln Arg Asn Gln Arg Leu Lys Ala Ala Asn 245	250	255
Phe Lys Ser Glu Pro Arg Trp Asp Phe Glu Glu Lys Tyr Ser Phe 260	265	270
Glu Ile Gly Gly Leu Gln Thr Thr Cys Pro Asp Ser Val Lys Ile 275	280	285
Lys Ala Ser Lys Ser Leu Trp Leu Gln Lys Leu Phe Leu Pro Asn 290	295	300
Leu Thr Leu Phe Leu Asp Ser Arg His Phe Asn Gln Ser Glu Trp 305	310	315
Asp Arg Leu Glu His Phe Ala Pro Pro Phe Gly Phe Met Glu Leu 320	325	330
Asn Tyr Ser Leu Val Gln Lys Val Val Thr Arg Phe Pro Pro Val 335	340	345
Pro Gln Gln Gln Leu Leu Leu Ala Ser Leu Pro Ala Gly Ser Leu 350	355	360
Arg Cys Ile Thr Cys Ala Val Val Gly Asn Gly Gly Ile Leu Asn 365	370	375
Asn Ser His Met Gly Gln Glu Ile Asp Ser His Asp Tyr Val Phe		

380	385	390
Arg Leu Ser Gly Ala Leu Ile Lys Gly Tyr Glu Gln Asp Val Gly 395	400	405
Thr Arg Thr Ser Phe Tyr Gly Phe Thr Ala Phe Ser Leu Thr Gln 410	415	420
Ser Leu Leu Ile Leu Gly Asn Arg Gly Phe Lys Asn Val Pro Leu 425	430	435
Gly Lys Asp Val Arg Tyr Leu His Phe Leu Glu Gly Thr Arg Asp 440	445	450
Tyr Glu Trp Leu Glu Ala Leu Leu Met Asn Gln Thr Val Met Ser 455	460	465
Lys Asn Leu Phe Trp Phe Arg His Arg Pro Gln Glu Ala Phe Arg 470	475	480
Glu Ala Leu His Met Asp Arg Tyr Leu Leu Leu His Pro Asp Phe 485	490	495
Leu Arg Tyr Met Lys Asn Arg Phe Leu Arg Ser Lys Thr Leu Asp 500	505	510
Gly Ala His Trp Arg Ile Tyr Arg Pro Thr Thr Gly Ala Leu Leu 515	520	525
Leu Leu Thr Ala Leu Gln Leu Cys Asp Gln Val Ser Ala Tyr Gly 530	535	540
Phe Ile Thr Glu Gly His Glu Arg Phe Ser Asp His Tyr Tyr Asp 545	550	555
Thr Ser Trp Lys Arg Leu Ile Phe Tyr Ile Asn His Asp Phe Lys 560	565	570
Leu Glu Arg Glu Val Trp Lys Arg Leu His Asp Glu Gly Ile Ile 575	580	585
Arg Leu Tyr Gln Arg Pro Gly Pro Gly Thr Ala Lys Ala Lys Asn 590	595	600

<210> 348

<211> 496

<212> DNA

<213> Homo sapiens

<400> 348

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tattcgataa atcagtgtac ttgacagtgt tatctgtcac ttat 496

<210> 349
<211> 91
<212> PRT
<213> Homo sapiens

<400> 349
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20 25 30
Leu Arg Met Lys Asp Lys Phe Leu Lys His Leu Thr Gly Pro Leu
35 40 45
Tyr Phe Ser Pro Lys Cys Ser Lys His Phe His Arg Leu Tyr His
50 55 60
Asn Thr Arg Asp Cys Thr Ile Pro Ala Tyr Tyr Lys Arg Cys Ala
65 70 75
Arg Leu Leu Thr Arg Leu Ala Val Ser Pro Val Cys Met Glu Asp
80 85 90

Lys

<210> 350
<211> 1141
<212> DNA
<213> Homo sapiens

<400> 350
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tgccggaccc gtcattcatcg gtactgtgc agggacccgtga ccttgcttat 300
caccgagagg cagcagaagg actgcctggc cttcagcccc aagaccatag 350
caggcatcgcc ctcagctgtg atcccttttgc ttgtgtggt tgccaccacc 400
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ccacagccgt gttcatgtt cccacccatgtt ggtcctgtc cccaatatcc 600

卷之三

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gctggggccc tactgttgtt ccctctgttgg ctgggggtttt gggaggagg 1050
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<210> 351
<211> 197
<212> PRT
<213> Homo sapiens

<400> 351
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Ala Leu Leu Val Leu Gly Ala Pro Leu Val Leu Ala Gly Glu Asp
      20          25          30
Cys Leu Trp Tyr Leu Asp Arg Asn Gly Ser Trp His Pro Gly Phe
      35          40          45
Asn Cys Glu Phe Phe Thr Phe Cys Cys Gly Thr Cys Tyr His Arg
      50          55          60
Tyr Cys Cys Arg Asp Leu Thr Leu Leu Ile Thr Glu Arg Gln Gln
      65          70          75
Lys His Cys Leu Ala Phe Ser Pro Lys Thr Ile Ala Gly Ile Ala
      80          85          90
Ser Ala Val Ile Leu Phe Val Ala Val Val Ala Thr Thr Ile Cys
      95          100         105
Cys Phe Leu Cys Ser Cys Cys Tyr Leu Tyr Arg Arg Arg Gln Gln
     110          115         120
Leu Gln Ser Pro Phe Glu Gly Gln Glu Ile Pro Met Thr Gly Ile
     125          130         135
Pro Val Gln Pro Val Tyr Pro Tyr Pro Gln Asp Pro Lys Ala Gly
     140          145         150
Pro Ala Pro Pro Gln Pro Gly Phe Met Tyr Pro Pro Ser Gly Pro
     155          160         165
Ala Pro Gln Tyr Pro Leu Tyr Pro Ala Gly Pro Pro Val Tyr Asp
     170          175         180

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Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro Ser Tyr Pro
185 190 195

Gly Ala

<210> 352
<211> 3226
<212> DNA
<213> Homo sapiens

<400> 352
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tctcttaact gtgtccactt ctcatgtgt tcagagactt gaagcatctc 200
caaaacgttag tggatggaca ccatttcctt ggaataaaaat acgacttctt 250
gagtagtcata tcccagtta ttatgtatctt ttatgtccatg caaaccttac 300
cacgctgacc ttctggggaa ccacgaaatg agaaatcaca gccagtcagc 350
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gaaatctgtt actgttgctt aaggactcat agaagaccat tttgtatgtca 800
ctgtgaatg gaggacccat ctgggtggct tcacatgttcc agatgtttag 850
tctgtcagca agataaccaa gagtgaggactt aagggttctgtt tttatgtgt 900
gccgacaaatg ataaatcaag cagattatgc actggatgttgc gcgggtactc 950
ttctagaattt ttatgtggat tattttcgcata taccgtatcc cctaccaaaa 1000
caagatctt ctgttatcc ctgttatcc ctgttgcttca tggaaaactg 1050
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cttctgcattt aagtaagctt ggcatcacaatg tgactgtggc ccatgaaactg 1150
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ggcttattaca ttgtgcatta cgaggatgtt ggatggact ctttgactgg 1950
cctttaaaaa ggaacacaca cagcagtcag cagtaatgtt cggcgaatgc 2000
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<210> 353
<211> 941
<212> PRT
<213> Homo sapiens

<400> 353
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20 25 30
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35 40 45
Pro Phe Pro Trp Asn Lys Ile Arg Leu Pro Glu Tyr Val Ile Pro
50 55 60
Val His Tyr Asp Leu Leu Ile His Ala Asn Leu Thr Thr Leu Thr
65 70 75
Phe Trp Gly Thr Thr Lys Val Glu Ile Thr Ala Ser Gln Pro Thr
80 85 90
Ser Thr Ile Ile His Ser His His Leu Gln Ile Ser Arg Ala
95 100 105
Thr Leu Arg Lys Gly Ala Gly Glu Arg Leu Ser Glu Glu Pro Leu
110 115 120
Gln Val Leu Glu His Pro Pro Gln Glu Gln Ile Ala Leu Leu Ala
125 130 135
Pro Glu Pro Leu Leu Val Gly Leu Pro Tyr Thr Val Val Ile His
140 145 150
Tyr Ala Gly Asn Leu Ser Glu Thr Phe His Gly Phe Tyr Lys Ser
155 160 165
Thr Tyr Arg Thr Lys Glu Gly Glu Leu Arg Ile Leu Ala Ser Thr
170 175 180
Gln Phe Glu Pro Thr Ala Ala Arg Met Ala Phe Pro Cys Phe Asp
185 190 195
Glu Pro Ala Phe Lys Ala Ser Phe Ser Ile Lys Ile Arg Arg Glu
200 205 210
Pro Arg His Leu Ala Ile Ser Asn Met Pro Leu Val Lys Ser Val

215	220	225
Thr Val Ala Glu Gly Leu Ile Glu Asp His Phe Asp Val Thr Val 230	235	240
Lys Met Ser Thr Tyr Leu Val Ala Phe Ile Ile Ser Asp Phe Glu 245	250	255
Ser Val Ser Lys Ile Thr Lys Ser Gly Val Lys Val Ser Val Tyr 260	265	270
Ala Val Pro Asp Lys Ile Asn Gln Ala Asp Tyr Ala Leu Asp Ala 275	280	285
Ala Val Thr Leu Leu Glu Phe Tyr Glu Asp Tyr Phe Ser Ile Pro 290	295	300
Tyr Pro Leu Pro Lys Gln Asp Leu Ala Ala Ile Pro Asp Phe Gln 305	310	315
Ser Gly Ala Met Glu Asn Trp Gly Leu Thr Thr Tyr Arg Glu Ser 320	325	330
Ala Leu Leu Phe Asp Ala Glu Lys Ser Ser Ala Ser Ser Lys Leu 335	340	345
Gly Ile Thr Val Thr Val Ala His Glu Leu Ala His Gln Trp Phe 350	355	360
Gly Asn Leu Val Thr Met Glu Trp Trp Asn Asp Leu Trp Leu Asn 365	370	375
Glu Gly Phe Ala Lys Phe Met Glu Phe Val Ser Val Ser Val Thr 380	385	390
His Pro Glu Leu Lys Val Gly Asp Tyr Phe Phe Gly Lys Cys Phe 395	400	405
Asp Ala Met Glu Val Asp Ala Leu Asn Ser Ser His Pro Val Ser 410	415	420
Thr Pro Val Glu Asn Pro Ala Gln Ile Arg Glu Met Phe Asp Asp 425	430	435
Val Ser Tyr Asp Lys Gly Ala Cys Ile Leu Asn Met Leu Arg Glu 440	445	450
Tyr Leu Ser Ala Asp Ala Phe Lys Ser Gly Ile Val Gln Tyr Leu 455	460	465
Gln Lys His Ser Tyr Lys Asn Thr Lys Asn Glu Asp Leu Trp Asp 470	475	480
Ser Met Ala Ser Ile Cys Pro Thr Asp Gly Val Lys Gly Met Asp 485	490	495
Gly Phe Cys Ser Arg Ser Gln His Ser Ser Ser Ser His Trp 500	505	510
His Gln Glu Gly Val Asp Val Lys Thr Met Met Asn Thr Trp Thr 515	520	525
Leu Gln Arg Gly Phe Pro Leu Ile Thr Ile Thr Val Arg Gly Arg		

530	535	540
Asn Val His Met Lys Gln Glu His Tyr Met Lys Gly Ser Asp Gly		
545	550	555
Ala Pro Asp Thr Gly Tyr Leu Trp His Val Pro Leu Thr Phe Ile		
560	565	570
Thr Ser Lys Ser Asn Met Val His Arg Phe Leu Leu Lys Thr Lys		
575	580	585
Thr Asp Val Leu Ile Leu Pro Glu Glu Val Glu Trp Ile Lys Phe		
590	595	600
Asn Val Gly Met Asn Gly Tyr Tyr Ile Val His Tyr Glu Asp Asp		
605	610	615
Gly Trp Asp Ser Leu Thr Gly Leu Leu Lys Gly Thr His Thr Ala		
620	625	630
Val Ser Ser Asn Asp Arg Ala Ser Leu Ile Asn Asn Ala Phe Gln		
635	640	645
Leu Val Ser Ile Gly Lys Leu Ser Ile Glu Lys Ala Leu Asp Leu		
650	655	660
Ser Leu Tyr Leu Lys His Glu Thr Glu Ile Met Pro Val Phe Gln		
665	670	675
Gly Leu Asn Glu Leu Ile Pro Met Tyr Lys Leu Met Glu Lys Arg		
680	685	690
Asp Met Asn Glu Val Glu Thr Gln Phe Lys Ala Phe Leu Ile Arg		
695	700	705
Leu Leu Arg Asp Leu Ile Asp Lys Gln Thr Trp Thr Asp Glu Gly		
710	715	720
Ser Val Ser Glu Gln Met Leu Arg Ser Glu Leu Leu Leu Ala		
725	730	735
Cys Val His Asn Tyr Gln Pro Cys Val Gln Arg Ala Glu Gly Tyr		
740	745	750
Phe Arg Lys Trp Lys Glu Ser Asn Gly Asn Leu Ser Leu Pro Val		
755	760	765
Asp Val Thr Leu Ala Val Phe Ala Val Gly Ala Gln Ser Thr Glu		
770	775	780
Gly Trp Asp Phe Leu Tyr Ser Lys Tyr Gln Phe Ser Leu Ser Ser		
785	790	795
Thr Glu Lys Ser Gln Ile Glu Phe Ala Leu Cys Arg Thr Gln Asn		
800	805	810
Lys Glu Lys Leu Gln Trp Leu Leu Asp Glu Ser Phe Lys Gly Asp		
815	820	825
Lys Ile Lys Thr Gln Glu Phe Pro Gln Ile Leu Thr Leu Ile Gly		
830	835	840
Arg Asn Pro Val Gly Tyr Pro Leu Ala Trp Gln Phe Leu Arg Lys		

845	850	855
Asn Trp Asn Lys Leu Val Gln Lys Phe Glu Leu Gly Ser Ser Ser		
860	865	870
Ile Ala His Met Val Met Gly Thr Thr Asn Gln Phe Ser Thr Arg		
875	880	885
Thr Arg Leu Glu Glu Val Lys Gly Phe Phe Ser Ser Leu Lys Glu		
890	895	900
Asn Gly Ser Gln Leu Arg Cys Val Gln Gln Thr Ile Glu Thr Ile		
905	910	915
Glu Glu Asn Ile Gly Trp Met Asp Lys Asn Phe Asp Lys Ile Arg		
920	925	930
Val Trp Leu Gln Ser Glu Lys Leu Glu Arg Met		
935	940	

<210> 354
<211> 1587
<212> DNA
<213> Homo sapiens

<400> 354
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gaacaccaggc tgccacacgcg gcttgggggtt ccaggacacg ttgatgctca 200
ttgagaggcg accccaaatggc agccgtgtc tctccaaagggtt ctgcacggag 250
gccaaaggacc aggagcccccg cgtcaactgag cacccggatgg gccccggcc 300
ctccctgatc tcctacacct tcgtgtccgc ccaggaggac ttctgcaaca 350
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ccccacacaca atcattcata tctacttcacc taacagcaac actggggaga 1500
gcctggagca tccggacttg ccctatggga gagggggacgc tggaggagtg 1550
actgcataata tctqataata cagaccctgt cttttca 1587

<210> 355
<211> 437
<212> PRT
<213> *Homo sapiens*

<400> 355
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 20 25 30
 His Val Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys
 35 40 45
 Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met
 50 55 60
 Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly
 65 70 75
 Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg
 80 85 90
 Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg
 95 100 105
 Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp
 110 115 120
 Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val
 125 130 135
 Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile
 140 145 150
 Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu

Homo sapiens

155	160	165
Arg Gly Gly Gly Ile Phe Ser Asn Leu Arg Val Gln Gly Cys Met		
170	175	180
Pro Gln Pro Gly Cys Asn Leu Leu Asn Gly Thr Gln Glu Ile Gly		
185	190	195
Pro Val Gly Met Thr Glu Asn Cys Asn Arg Lys Asp Phe Leu Thr		
200	205	210
Cys His Arg Gly Thr Thr Ile Met Thr His Gly Asn Leu Ala Gln		
215	220	225
Glu Pro Thr Asp Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val		
230	235	240
Gly Gln Val Cys Gln Glu Thr Leu Leu Ile Asp Val Gly Leu		
245	250	255
Thr Ser Thr Leu Val Gly Thr Lys Gly Cys Ser Thr Val Gly Ala		
260	265	270
Gln Asn Ser Gln Lys Thr Thr Ile His Ser Ala Pro Pro Gly Val		
275	280	285
Leu Val Ala Ser Tyr Thr His Phe Cys Ser Ser Asp Leu Cys Asn		
290	295	300
Ser Ala Ser Ser Ser Ser Val Leu Leu Asn Ser Leu Pro Pro Gln		
305	310	315
Ala Ala Pro Val Pro Gly Asp Arg Gln Cys Pro Thr Cys Val Gln		
320	325	330
Pro Leu Gly Thr Cys Ser Ser Gly Ser Pro Arg Met Thr Cys Pro		
335	340	345
Arg Gly Ala Thr His Cys Tyr Asp Gly Tyr Ile His Leu Ser Gly		
350	355	360
Gly Gly Leu Ser Thr Lys Met Ser Ile Gln Gly Cys Val Ala Gln		
365	370	375
Pro Ser Ser Phe Leu Leu Asn His Thr Arg Gln Ile Gly Ile Phe		
380	385	390
Ser Ala Arg Glu Lys Arg Asp Val Gln Pro Pro Ala Ser Gln His		
395	400	405
Glu Gly Gly Ala Glu Gly Leu Glu Ser Leu Thr Trp Gly Val		
410	415	420
Gly Leu Ala Leu Ala Pro Ala Leu Trp Trp Gly Val Val Cys Pro		
425	430	435
Ser Cys		

<210> 356
<211> 1238
<212> DNA
<213> Homo sapiens

<400> 356
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tcagccctggc cttccctgtca ctgctggcat ctggacatcc tcagccggct 150
ggcgatgacg cctgctctgt gcagatcctc gtcctggcc tcaaaggaga 200
tgcgggagag aaggagaca aaggcgcccc cgacggcct ggaagagtgc 250
gccccacggg agaaaaaggaa gacatggggg acaaaggaca gaaaggcagt 300
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ccattggggg ccccacatgt ccctgcaggg ttggcaggga cagagccag 950
accatgggtc cagccaggaa gctgtccctc tggtaagggt ggaggctcac 1000
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aaaatgaaag tggcctggg gtgtgtctc tgagaagca gagtttcatt 1100
acctgtattt tagccccaaat gtcatattgt aattattacc cagaattgtct 1150
cttccataaa gcttgcctt tttccaaagg tataacaataa aatcttaag 1200
tagtgcagta gttaaatccaa aaaaaaaaaa aaaaaaaaa 1238

<210> 357

<211> 271

<212> PRT

<213> Homo sapiens

<400> 357

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Phe	Leu	Ser	Leu	Leu	Pro	Ser	Gly	His	Pro	Gln	Pro	Ala	Gly	Asp
20								25						30

卷之三

Asp	Ala	Cys	Ser	Val	Gln	Ile	Leu	Val	Pro	Gly	Leu	Lys	Gly	Asp
				35					40					45
Ala	Gly	Glu	Lys	Gly	Asp	Lys	Gly	Ala	Pro	Gly	Arg	Pro	Gly	Arg
				50					55					60
Val	Gly	Pro	Thr	Gly	Glu	Lys	Gly	Asp	Met	Gly	Asp	Lys	Gly	Gln
				65					70					75
Lys	Gly	Ser	Val	Gly	Arg	His	Gly	Lys	Ile	Gly	Pro	Ile	Gly	Ser
				80					85					90
Lys	Gly	Glu	Lys	Gly	Asp	Ser	Gly	Asp	Ile	Gly	Pro	Pro	Gly	Pro
				95					100					105
Asn	Gly	Glu	Pro	Gly	Leu	Pro	Cys	Glu	Cys	Ser	Gln	Leu	Arg	Lys
				110					115					120
Ala	Ile	Gly	Glu	Met	Asp	Asn	Gln	Val	Ser	Gln	Leu	Thr	Ser	Glu
				125					130					135
Leu	Lys	Phe	Ile	Lys	Asn	Ala	Val	Ala	Gly	Val	Arg	Glu	Thr	Glu
				140					145					150
Ser	Lys	Ile	Tyr	Leu	Leu	Val	Lys	Glu	Glu	Lys	Arg	Tyr	Ala	Asp
				155					160					165
Ala	Gln	Leu	Ser	Cys	Gln	Gly	Arg	Gly	Gly	Thr	Leu	Ser	Met	Pro
				170					175					180
Lys	Asp	Glu	Ala	Ala	Asn	Gly	Leu	Met	Ala	Ala	Tyr	Leu	Ala	Gln
				185					190					195
Ala	Gly	Leu	Ala	Arg	Val	Phe	Ile	Gly	Ile	Asn	Asp	Leu	Glu	Lys
				200					205					210
Glu	Gly	Ala	Phe	Val	Tyr	Ser	Asp	His	Ser	Pro	Met	Arg	Thr	Phe
				215					220					225
Asn	Lys	Trp	Arg	Ser	Gly	Glu	Pro	Asn	Asn	Ala	Tyr	Asp	Glu	Glu
				230					235					240
Asp	Cys	Val	Glu	Met	Val	Ala	Ser	Gly	Gly	Trp	Asn	Asp	Val	Ala
				245					250					255
Cys	His	Thr	Thr	Met	Tyr	Phe	Met	Cys	Glu	Phe	Asp	Lys	Glu	Asn
				260					265					270

Met

<210> 358
<211> 972
<212> DNA
<213> *Homo sapiens*

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gagcaccggc agcaccaggc tgtagggga gcaggcagcg gtccttagcca 100  
  
atcccttgat cctgcacagac cacccagcccc ccggcacacaga gtcgtccac 150
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卷之三

aggccatcatgc aggatcatgc tgctattcac agccatctgc gccttcagcc 200
tagctcgag ctttggggct gtctgttaagg agccacagga ggaggtgttt 250
cctggcgaaa gcccggcaaa gagggatcca gatcttacc agtgtctcca 300
gagactcttc aaaaggccact catctctggaa gggattgtc aaaggccctga 350
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atgcattgact tctttgtggg acttatgggc aagaggagcc tccagccaga 450
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cctcaacaat aaaggatttt tgcatatgaa aaaaaaaaaa aaaaaaaaaa 950
aaaaaaaaaa aaaaaaaaaa aa 972

<210> 359
<211> 135
<212> PRT
<213> *Homo sapiens*

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<400> 359
Met Arg Ile Met Leu Leu Phe Thr Ala Ile Leu Ala Phe Ser Leu
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Ala Gln Ser Phe Gly Ala Val Cys Lys Glu Pro Gln Glu Glu Val
      20          25          30
Val Pro Gly Gly Gly Arg Ser Lys Arg Asp Pro Asp Leu Tyr Gln
      35          40          45
Leu Leu Gln Arg Leu Phe Lys Ser His Ser Ser Leu Glu Gly Leu
      50          55          60
Leu Lys Ala Leu Ser Gln Ala Ser Thr Asp Pro Lys Glu Ser Thr
      65          70          75
Ser Pro Glu Lys Arg Asp Met His Asp Phe Phe Val Gly Leu Met
      80          85          90
Gly Lys Arg Ser Val Gln Pro Glu Gly Lys Thr Gly Pro Phe Leu
      95          100         105
Pro Ser Val Arg Val Pro Arg Pro Leu His Pro Asn Gln Leu Gly
      110         115         120

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Ser Thr Gly Lys Ser Ser Leu Gly Thr Glu Glu Gln Arg Pro Leu
125 130 135

<210> 360
<211> 1738
<212> DNA
<213> Homo sapiens

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agctctgccc caggagccca ggctgcggcc tgagtcccat agttgctgca 200
ggagtgggagc catgagctgc gtccctgggt gtgtcatccc cttggggctg 250
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<210> 361

<211> 159

<212> PRT

<213> Homo sapiens

<400> 361

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Leu	Val	Cys	Gly	Ser	Gln	Gly	Tyr	Leu	Leu	Pro	Asn	Val	Thr	Leu
	20							25						30
Leu	Glu	Glu	Leu	Leu	Ser	Lys	Tyr	Gln	His	Asn	Glu	Ser	His	Ser
	35							40						45
Arg	Val	Arg	Arg	Ala	Ile	Pro	Arg	Glu	Asp	Lys	Glu	Glu	Ile	Leu
	50							55						60
Met	Leu	His	Asn	Lys	Leu	Arg	Gly	Gln	Val	Gln	Pro	Gln	Ala	Ser
	65							70						75
Asn	Met	Glu	Tyr	Met	Val	Ser	Ala	Gly	Ser	Gly	Arg	Arg	Gly	Trp
	80							85						90
His	Arg	Gly	Trp	Gly	Leu	Gly	His	Gln	Pro	Ala	Leu	Phe	Pro	Ser
	95							100						105
Gln	Leu	Cys	Ser	Pro	Ala	Ser	Ala	Cys	Asp	Gly	Trp	Leu	Arg	Val
	110							115						120
Ser	Ser	Gly	Arg	Gly	Gly	Ser	Arg	Leu	Cys	Ser	Val	Leu	Phe	Val
	125							130						135
Cys	Phe	Glu	Thr	Gly	Ser	His	Ser	Ala	Thr	Asp	Ala	Gly	Val	Gln
	140							145						150
Trp	His	Asn	Arg	His	Ala	Leu	Lys	Pro						
	155													

<210> 362

<211> 422

<212> DNA

<213> Homo sapiens

<400> 362

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gagtctttc tgacaaattc ctcctatgag tccagttcc tggattgtct 200
tggaaaagctc tgcctccctcc tccatctcc ttcaaggacc agcgtcaccc 250
tcccatatgc aagatctcaa caccatgttg tctgaaacac atgacagcca 300
ttgaagcctg tgccttctt ggccggggct tttgggggg ggatgcagga 350
ggcaggcccc gaccctgtct ttcagcaggc ccccacccctc ctgagtgcca 400
ataaataaaa ttcggtatgc tg 422

<210> 363
<211> 78
<212> PRT
<213> Homo sapiens

<400> 363
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20 25 30
Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu
35 40 45
Glu Leu Leu Glu Lys Leu Cys Leu Leu His Leu Pro Ser Gly
50 55 60
Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val
65 70 75

Cys Asn Thr

<210> 364
<211> 826
<212> DNA
<213> Homo sapiens

<400> 364
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acaattaact gttaggattg cagttatgtat tggatattat ttaattctgt 150
ttctgtatgtt gggccctcc actgtgttct gtgtgttatt aatatttacc 200
attgcagaag cttcatttcg tggatggaaat gaatgttag tggatctgt 250
cctttacgc atatgttaca aattatctgg agttcctaataat caatgcagag 300
ttccccctcc ctccgattgt tctaaataat tggatgttctt ctgtgtgga 350
aaaaggcatg tatttaaatc tggatgttcc tcaaccatct ttagttggga 400
aaggcccttg aaaggccatg gaaataactt tttttttctt tggcactaat 450

caagttagtg ttacctttc acttagtagg atgtgttggt acgctagtaa 500
aatagaaacc tgtgtttatt ctcaggattt ttagaaacaa cagccatcat 550
tttattttat gtgtgttgc ttggctgtat tcataaaatta tatattttgg 600
gctatcaaattt attacttcat tcaatataaa taacaatagt agaagtgtt 650
tacttagata tgctttctag ttgcatttc tcagcctatg taagactact 700
tttgttaat agcctttgaa atttacagta ctgtctctt actatcttca 750
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accagaataa aagttcatat ctaccc 826

<210> 365
<211> 67
<212> PRT
<213> Homo sapiens

<400> 365
Met Ile Gly Tyr Tyr Leu Ile Leu Phe Leu Met Trp Gly Ser Ser
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Thr Val Phe Cys Val Leu Leu Ile Phe Thr Ile Ala Glu Ala Ser
20 25 30
Phe Ser Val Glu Asn Glu Cys Leu Val Asp Leu Cys Leu Leu Arg
35 40 45
Ile Cys Tyr Lys Leu Ser Gly Val Pro Asn Gln Cys Arg Val Pro
50 55 60
Leu Pro Ser Asp Cys Ser Lys
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<210> 366
<211> 2475
<212> DNA
<213> Homo sapiens

<400> 366
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ttttcgagga tggatgtggc ccttcgagga gcttctgcat tgctgggtct 150
gttccttgcg gctttctgc ccccccgcg gtgtaccccg gacccagcca 200
tggtgattt catctaccag cgctttcgag tcttggagca agggctggaa 250
aaatgtaccc aagcaacgag ggcatacatt caagaattcc aagagttctc 300
aaaaaaataa tctgtcatgc tggaaagatg tcagacctac acaagtgggt 350
acaagagtgcc agtgggtaaat ttggcactga gagttgaacg tgcccaacgg 400
gagattgact acataacaata ccttcgagag gctgacggat gcacgtatc 450
agaggacaag acactggcag aaatgttgc ccaagaagct gaagaagaga 500

卷之三

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ccgaaaacaa cactgtttgg gaatttgc aaacatacgcc attcatggag 700
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<210> 367
<211> 402
<212> PRT
<213> Homo sapiens

<400> 367
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20 25 30
Met Val His Tyr Ile Tyr Gln Arg Phe Arg Val Leu Glu Gln Gly
35 40 45
Leu Glu Lys Cys Thr Gln Ala Thr Arg Ala Tyr Ile Gln Glu Phe
50 55 60
Gln Glu Phe Ser Lys Asn Ile Ser Val Met Leu Gly Arg Cys Gln
65 70 75
Thr Tyr Thr Ser Glu Tyr Lys Ser Ala Val Gly Asn Leu Ala Leu
80 85 90
Arg Val Glu Arg Ala Gln Arg Glu Ile Asp Tyr Ile Gln Tyr Leu
95 100 105
Arg Glu Ala Asp Glu Cys Ile Val Ser Glu Asp Lys Thr Leu Ala
110 115 120
Glu Met Leu Leu Gln Glu Ala Glu Glu Glu Lys Lys Ile Arg Thr
125 130 135
Leu Leu Asn Ala Ser Cys Asp Asn Met Leu Met Gly Ile Lys Ser
140 145 150
Leu Lys Ile Val Lys Lys Met Met Asp Thr His Gly Ser Trp Met
155 160 165
Lys Asp Ala Val Tyr Asn Ser Pro Lys Val Tyr Leu Leu Ile Gly
170 175 180
Ser Arg Asn Asn Thr Val Trp Glu Phe Ala Asn Ile Arg Ala Phe
185 190 195
Met Glu Asp Asn Thr Lys Pro Ala Pro Arg Lys Gln Ile Leu Thr
200 205 210

HOMO SAPIENS

Leu Ser Trp Gln Gly Thr Gly Gln Val Ile Tyr Lys Gly Phe Leu
215 220 225
Phe Phe His Asn Gln Ala Thr Ser Asn Glu Ile Ile Lys Tyr Asn
230 235 240
Leu Gln Lys Arg Thr Val Glu Asp Arg Met Leu Leu Pro Gly Gly
245 250 255
Val Gly Arg Ala Leu Val Tyr Gln His Ser Pro Ser Thr Tyr Ile
260 265 270
Asp Leu Ala Val Asp Glu His Gly Leu Trp Ala Ile His Ser Gly
275 280 285
Pro Gly Thr His Ser His Leu Val Leu Thr Lys Ile Glu Pro Gly
290 295 300
Thr Leu Gly Val Glu His Ser Trp Asp Thr Pro Cys Arg Ser Gln
305 310 315
Asp Ala Glu Ala Ser Phe Leu Leu Cys Gly Val Leu Tyr Val Val
320 325 330
Tyr Ser Thr Gly Gly Gln Gly Pro His Arg Ile Thr Cys Ile Tyr
335 340 345
Asp Pro Leu Gly Thr Ile Ser Glu Glu Asp Leu Pro Asn Leu Phe
350 355 360
Phe Pro Lys Arg Pro Arg Ser His Ser Met Ile His Tyr Asn Pro
365 370 375
Arg Asp Lys Gln Leu Tyr Ala Trp Asn Glu Gly Asn Gln Ile Ile
380 385 390
Tyr Lys Leu Gln Thr Lys Arg Leu Pro Leu Lys
395 400

<210> 368
<211> 2281
<212> DNA
<213> Homo sapiens

<400> 368
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ctggccctga tggcgacggc ggccggtagcc cgccgggtggc tgccgcggg 150
ggaggagagg agcggccggc cccgcctgccaaa aaaaagaaat ggattttcac 200
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atgtgaaggt ttgggaagtc tgctttggaa agaaggggaa gttccaggag 850
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gtcatgaaag tggtaaaagt gggaaaccagt gtgtttgaa accaaattag 2050

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 cctctttca gttcatcaag ttcatcagat atttgagtgc ccactctgt 2200
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2281

<210> 369
 <211> 447
 <212> PRT
 <213> Homo sapiens

<400> 369
 Met Glu Leu Ser Gln Met Ser Glu Leu Met Gly Leu Ser Val Leu
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 Leu Gly Leu Leu Ala Leu Met Ala Thr Ala Ala Val Ala Arg Gly
 20 25 30
 Trp Leu Arg Ala Gly Glu Glu Arg Ser Gly Arg Pro Ala Cys Gln
 35 40 45
 Lys Ala Asn Gly Phe Pro Pro Asp Lys Ser Ser Gly Ser Lys Lys
 50 55 60
 Gln Lys Gln Tyr Gln Arg Ile Arg Lys Glu Lys Pro Gln Gln His
 65 70 75
 Asn Phe Thr His Arg Leu Leu Ala Ala Leu Lys Ser His Ser
 80 85 90
 Gly Asn Ile Ser Cys Met Asp Phe Ser Ser Asn Gly Lys Tyr Leu
 95 100 105
 Ala Thr Cys Ala Asp Asp Arg Thr Ile Arg Ile Trp Ser Thr Lys
 110 115 120
 Asp Phe Leu Gln Arg Glu His Arg Ser Met Arg Ala Asn Val Glu
 125 130 135
 Leu Asp His Ala Thr Leu Val Arg Phe Ser Pro Asp Cys Arg Ala
 140 145 150
 Phe Ile Val Trp Leu Ala Asn Gly Asp Thr Leu Arg Val Phe Lys
 155 160 165
 Met Thr Lys Arg Glu Asp Gly Gly Tyr Thr Phe Thr Ala Thr Pro
 170 175 180
 Glu Asp Phe Pro Lys Lys His Lys Ala Pro Val Ile Asp Ile Gly
 185 190 195
 Ile Ala Asn Thr Gly Lys Phe Ile Met Thr Ala Ser Ser Asp Thr
 200 205 210
 Thr Val Leu Ile Trp Ser Leu Lys Gly Gln Val Leu Ser Thr Ile
 215 220 225
 Asn Thr Asn Gln Met Asn Asn Thr His Ala Ala Val Ser Pro Cys
 230 235 240

Gly Arg Phe Val Ala Ser Cys Gly Phe Thr Pro Asp Val Lys Val
245 250 255

Trp Glu Val Cys Phe Gly Lys Lys Gly Glu Phe Gln Glu Val Val
260 265 270

Arg Ala Phe Glu Leu Lys Gly His Ser Ala Ala Val His Ser Phe
275 280 285

Ala Phe Ser Asn Asp Ser Arg Arg Met Ala Ser Val Ser Lys Asp
290 295 300

Gly Thr Trp Lys Leu Trp Asp Thr Asp Val Glu Tyr Lys Lys Lys
305 310 315

Gln Asp Pro Tyr Leu Leu Lys Thr Gly Arg Phe Glu Glu Ala Ala
320 325 330

Gly Ala Ala Pro Cys Arg Leu Ala Leu Ser Pro Asn Ala Gln Val
335 340 345

Leu Ala Leu Ala Ser Gly Ser Ser Ile His Leu Tyr Asn Thr Arg
350 355 360

Arg Gly Glu Lys Glu Glu Cys Phe Glu Arg Val His Gly Glu Cys
365 370 375

Ile Ala Asn Leu Ser Phe Asp Ile Thr Gly Arg Phe Leu Ala Ser
380 385 390

Cys Gly Asp Arg Ala Val Arg Leu Phe His Asn Thr Pro Gly His
395 400 405

Arg Ala Met Val Glu Glu Met Gln Gly His Leu Lys Arg Ala Ser
410 415 420

Asn Glu Ser Thr Arg Gln Arg Leu Gln Gln Leu Thr Gln Ala
425 430 435

Gln Glu Thr Leu Lys Ser Leu Gly Ala Leu Lys Lys
440 445

<210> 370

<211> 1415

<212> DNA

<213> Homo sapiens

<400> 370
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ccacgcgagt ctcaatcatg ctccctctag taactgtgtc tgactgtgtc 150
gtgatcacag gggcctgtga gcgggatgtc cagtgtgggg caggcacctg 200
ctgtgccatc agcctgtggc ttcgagggtc gcggtatgtc accccgcgtgg 250
ggcgaaaagg cgaggagtgc cacccccggca gccacaagggt ccccttc 300
agggaaacgc a gacccacac ctgtccttgc ttgcccacc tgctgtgtc 350
caggttcccc gacggcagggt acccgctgtc catggacttg aagaacatca 400

attttttagc gcttgcctgg ttcaggata cccaccatcc ttttcttgc 450
cacagcctgg attttattt ctgcatgaa acccagctcc catgactctc 500
ccagtcctca cactgactac cctgatctc cttgtctagt acgcacatat 550
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tggtaactc cttagttca gaccacagac tcaagattgg ctttccctc 950
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aatcagcccc ctgaagactc tggtccctgtt cagcctgtgg ctgtggcc 1050
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accacactt accagttaac cactgaaagcc cccaaattccc acagctttc 1150
cattaaatgt caaatgggtt tggttcaatc taatctgtata ttgacatatt 1200
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ctgagagcag gttgggtact ttgaggaggc cagtcctctgtt ccagattgg 1300
ggggggagca agggacagggc agcaggccag gggctgaaag gggcactgtat 1350
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caccaactga aaaaa 1415

<210> 371

<211> 105

<212> PRT

<213> Homo sapiens

<400> 371

Met	Arg	Gly	Ala	Thr	Arg	Val	Ser	Ile	Met	Leu	Leu	Leu	Val	Thr
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Val	Ser	Asp	Cys	Ala	Val	Ile	Thr	Gly	Ala	Cys	Glu	Arg	Asp	Val
					20					25				30
Gln	Cys	Gly	Ala	Gly	Thr	Cys	Cys	Ala	Ile	Ser	Leu	Trp	Leu	Arg
									35					45
Gly	Leu	Arg	Met	Cys	Thr	Pro	Leu	Gly	Arg	Glu	Gly	Glu	Cys	
				50					55					60
His	Pro	Gly	Ser	His	Lys	Val	Pro	Phe	Phe	Arg	Lys	Arg	Lys	His
					65				70					75

His Thr Cys Pro Cys Leu Pro Asn Leu Leu Cys Ser Arg Phe Pro
80 85 90

Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu Lys Asn Ile Asn Phe
95 100 105

<210> 372

<211> 1281

<212> DNA

<213> Homo sapiens

<400> 372

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aaaaatgtctt tcctccagga cccaaagttc ttccacatgg ggatgtggtc 100

catttgtca ggagccctgg gggctgtgc ctggcattt ctgtttgcca 150

acacagacgt gtttctgtcc aagccccaga aagcccccgt ggagtacctg 200

gaggatatacg acctgaaaac actggagaag gaacaagga ctttcaaagc 250

aaaggagcta tggaaaaaaa atggagctgt gattatggcc gtgcggggc 300

caggctgttt cctctgtcga gaggaaatgtc cggatctgtc ctccctgaaa 350

acatgttgg accagctggg cgtccccctc tatcgttg taaaggagca 400

catcaggact gaagtgaagg atttccagcc ttatccaaa ggagaaatct 450

tcctggatga aaagaaaaag ttctatgtgc cacaaggcg gaagatgtg 500

tttatggat ttatccgtct gggagttgtgg tacaacttct tccgagctg 550

gaacggaggc ttctctggaa acctggaaagg agaaggcttc atccctgggg 600

gagtttcgt ggtggatca ggaaggcagg gcattttct tgagcaccga 650

aaaaagaat ttggagacaa agtaaaccta ctttctgtc tgaaagctgc 700

taagatgtac aaaccacaga ctttggcctc agagaaaaaa tgattgtgt 750

aaactgccccca gctcaggat aaccaggac attcacctgt gttcatggga 800

tgtattgttt ccactctgtc ccctaaggag tgagaaaccc atttataactc 850

tactctcgt atggatttatt aatgtatttt aatattctgt ttaggcccac 900

taaggcaaaa tagccccaaa acaagactga caaaaatctg aaaaactaat 950

gaggattatt aagctaaaaac ctggaaata ggaggctta aattgactgc 1000

caggctgggt gcagtggcctc acacctgtaa tcccagact ttgggaggcc 1050

aagggtgacca agtcaacttga ggtcgaggat tcgagaccag cctgagcaac 1100

atggcgaaac cccgtctcta ctaaaaatac aaaaatcacc cgggtgtgg 1150

ggcaggcacc ttagtccca gctaccgggg aggctgaggc aggagaatca 1200

cttgaacctg ggaggtggag gttcggtga gctgagatca caccactgt 1250

ttccagctcg ggtgactgag actcttaacta a 1281

<210> 373
<211> 229
<212> PRT
<213> Homo sapiens

<400> 373
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp
1 5 10 15
Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu
20 25 30
Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala
35 40 45
Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu
50 55 60
Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala
65 70 75
Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu
80 85 90
Glu Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu
95 100 105
Gly Val Pro Leu Tyr Ala Val Val Lys Glu His Ile Arg Thr Glu
110 115 120
Val Lys Asp Phe Gln Pro Tyr Phe Lys Gly Glu Ile Phe Leu Asp
125 130 135
Glu Lys Lys Lys Phe Tyr Gly Pro Gln Arg Arg Lys Met Met Phe
140 145 150
Met Gly Phe Ile Arg Leu Gly Val Trp Tyr Asn Phe Phe Arg Ala
155 160 165
Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly Glu Gly Phe Ile
170 175 180
Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln Gly Ile Leu
185 190 195
Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn Leu Leu
200 205 210
Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu Ala
215 220 225
Ser Glu Lys Lys

<210> 374
<211> 744
<212> DNA
<213> Homo sapiens

<400> 374
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gccccatggc gggcgagcgc gagaagcccc ttccctcgccg ctgccaaccc 150
gccacccagg ccatggcgaa ccccgccgtg gggctgcttc tggcgctggg 200
cctgcccgttc ctgctggccc gctggggccg agcctgggg caaatacaga 250
ccacttgc aaatgagaat agcaactgttt tgccctcata caccagctcc 300
agctccgatg gcaacacctcg tccggaaagcc atcaactgcta tcatcggtt 350
cttctccctc ttggctgcct tgctcctggc tggggctg gcaactgttg 400
tgccgaagct tcgggagaag cgccagacgg agggcaccta ccggcccaagt 450
agcgaggaggc agtttccca tgcaagccag gccccggccc ctcaggactc 500
caaggagacg gtgcaggggct gctgccccat cttaggtcccc tctccctgcat 550
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ggcagtcag atccaccccg tgcttaatag cagggaaagaa ggtacttcaa 650
agactctgcc octgagggtca agagaggatg gggctattca ctttttatata 700
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<210> 375

<211> 123

<212> PRT

<213> Homo sapiens

<400> 375

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Phe	Leu	Leu	Ala	Arg	Trp	Gly	Arg	Ala	Trp	Gly	Gln	Ile	Gln	Thr
				20					25					30
Thr	Ser	Ala	Asn	Glu	Asn	Ser	Thr	Val	Leu	Pro	Ser	Ser	Thr	Ser
				35					40					45
Ser	Ser	Ser	Asp	Gly	Asn	Leu	Arg	Pro	Glu	Ala	Ile	Thr	Ala	Ile
				50					55					60
Ile	Val	Val	Phe	Ser	Leu	Leu	Ala	Ala	Leu	Leu	Leu	Ala	Val	Gly
				65					70					75
Leu	Ala	Leu	Leu	Val	Arg	Lys	Leu	Arg	Glu	Lys	Arg	Gln	Thr	Glu
				80					85					90
Gly	Thr	Tyr	Arg	Pro	Ser	Ser	Glu	Glu	Gln	Phe	Ser	His	Ala	Ala
				95					100					105
Glu	Ala	Arg	Ala	Pro	Gln	Asp	Ser	Lys	Glu	Thr	Val	Gln	Gly	Cys
				110					115					120

Leu Pro Ile

<210> 376

<211> 713

<212> DNA

<213> Homo sapiens

<400> 376
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aacatttggg ttttgggatt ttaatttc aacacagcag aatgcattt 100
tttctgtcac tattattattt gttggatgt gaagcttggatccaa 150
ttcaggaaagc aacacattgg agaatggcta ctttctatca agaaaataag 200
agaaccacag tcaacccaca caatcatctt tagaagacag tgtgactct 250
accaaagctg tcaaaaccac aggcaaggc atagttaaag gacggatct 300
tgactcaaga gggtaattc ttgggtctga agcctgggc aggggtgtaa 350
agaaaaacac ttagattcaa tgattgtaaa ttttaaggca atacacatat 400
tagtattacc tttagtgaat gtatccctgt catatataca ataaggtgaa 450
attataagta ccctatgcag ttggctggac agttctaaat tggactttat 500
taatttttaa aatcagtaac tgattttca ctggctatgt gcttagatct 550
acaggagatc atataatttg atacaataa aagaaaagtg ttctctcccc 600
ttacagaattt gacattttaa atgcgatatac gtttagaatag gaaatatgac 650
attagaaagg aagaatgaca gggagaaagg aaagaaggaa aaatgttgcc 700
aaggaaaaaaa aaa 713

<210> 377

<211> 90

<212> PRT

<213> Homo sapiens

<400> 377
Met Thr Phe Phe Leu Ser Leu Leu Leu Leu Val Cys Glu Ala
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Ile Trp Arg Ser Asn Ser Gly Ser Asn Thr Leu Glu Asn Gly Tyr
20 25 30
Phe Leu Ser Arg Asn Lys Glu Asn His Ser Gln Pro Thr Gln Ser
35 40 45
Ser Leu Glu Asp Ser Val Thr Pro Thr Lys Ala Val Lys Thr Thr
50 55 60
Gly Lys Gly Ile Val Lys Gly Arg Asn Leu Asp Ser Arg Gly Leu
65 70 75
Ile Leu Gly Ala Glu Ala Trp Gly Arg Gly Val Lys Lys Asn Thr
80 85 90

<210> 378

<211> 3265

<212> DNA

<213> Homo sapiens

<400> 378
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cctcttagtt ctgtgcctgc tgacccagtc aaataacttcc ttcatattaagc 100
tgaataataa tggcttggaa gatattgtca ttgttataga tccttagtgt 150
ccagaagatg aaaaaataat tgaacaataa gaggatatgg tgactacagc 200
ttctacgtac ctgtttgaag ccacagaaaa aagattttt ttcaaaaatg 250
tatctatatt aattcctgag aatttggagg aaaaatcctca gtacaaaagg 300
ccaaacatg aaaaccataa acatgctgat gttatagtt caccacctac 350
actcccaggt agagatgaac catacaccaa gcagttcaca gaatgtggag 400
agaaaggcgta atacattcac ttcacccctg accttctact tggaaaaaaa 450
caaataaat atggaccacc aggcaaaactg tttgtccatg agtgggctca 500
cctccgggtgg ggagtgtttt atgagttacaa tgaagatcg ctttctacc 550
gtgctaagtca aaaaaaaatc gaagcaacaa ggtgtccgc aggtatctct 600
gttagaaaaata gagtttataa gtgtcaagga ggcagctgca ttagtagac 650
atgcagaatt gattctacaa caaaactgta tggaaaagat tgtcaattct 700
ttcctgataa agtacaaaca gaaaaagcat ccataatgtt tatgcaaagt 750
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gatgaagcag taatagagat gagcaagata acaggaggaa gtcattttta 1400
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tgcctcccaag tatttctctc tggatccccat gttggaaacaat aatggaaaat 1650

DRAFT - 15/03/2009

ttcacagtgg atgcaacttc caaaatggcc tatctcagta ttccaggaac 1700
tgcaaagggt ggcacttggg catacaatct tcaagccaaa gcgaacccag 1750
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ccaatcacag tgaatgtcaa aatgaataag gacgtaaaca gtttccccag 1850
ccaaatgatt gtttacgcag aaattctaca aggatatgtta cctgttcttg 1900
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aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3250

TOPXX-HSFR660

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<210> 379
<211> 919
<212> PRT
<213> Homo sapiens<400> 379
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Leu His Gln Ser Asn Thr Ser Phe Ile Lys Leu Asn Asn Asn Gly
20 25 30
Phe Glu Asp Ile Val Ile Val Ile Asp Pro Ser Val Pro Glu Asp
35 40 45
Glu Lys Ile Ile Glu Gln Ile Glu Asp Met Val Thr Thr Ala Ser
50 55 60
Thr Tyr Leu Phe Glu Ala Thr Glu Lys Arg Phe Phe Phe Lys Asn
65 70 75
Val Ser Ile Leu Ile Pro Glu Asn Trp Lys Glu Asn Pro Gln Tyr
80 85 90
Lys Arg Pro Lys His Glu Asn His Lys His Ala Asp Val Ile Val
95 100 105
Ala Pro Pro Thr Leu Pro Gly Arg Asp Glu Pro Tyr Thr Lys Gln
110 115 120
Phe Thr Glu Cys Gly Glu Lys Gly Glu Tyr Ile His Phe Thr Pro
125 130 135
Asp Leu Leu Leu Gly Lys Lys Gln Asn Glu Tyr Gly Pro Pro Gly
140 145 150
Lys Leu Phe Val His Glu Trp Ala His Leu Arg Trp Gly Val Phe
155 160 165
Asp Glu Tyr Asn Glu Asp Gln Pro Phe Tyr Arg Ala Lys Ser Lys
170 175 180
Lys Ile Glu Ala Thr Arg Cys Ser Ala Gly Ile Ser Gly Arg Asn
185 190 195
Arg Val Tyr Lys Cys Gln Gly Gly Ser Cys Leu Ser Arg Ala Cys
200 205 210
Arg Ile Asp Ser Thr Thr Lys Leu Tyr Gly Lys Asp Cys Gln Phe
215 220 225
Phe Pro Asp Lys Val Gln Thr Glu Lys Ala Ser Ile Met Phe Met
230 235 240
Gln Ser Ile Asp Ser Val Val Glu Phe Cys Asn Glu Lys Thr His
245 250 255
Asn Gln Glu Ala Pro Ser Leu Gln Asn Ile Lys Cys Asn Phe Arg
260 265 270
Ser Thr Trp Glu Val Ile Ser Asn Ser Glu Asp Phe Lys Asn Thr

275

280

285

Ile Pro Met Val Thr Pro Pro Pro Pro Pro	290	295	Leu
Lys Ile Ser Gln Arg Ile Val Cys Leu Val	305	310	Gly
Ser Met Gly Gly Lys Asp Arg Leu Asn Arg	320	325	Met Asn Gln Ala Ala
Lys His Phe Leu Leu Gln Thr Val Glu Asn	335	340	Gly Ser Trp Val Gly
Met Val His Phe Asp Ser Thr Ala Thr Ile	350	355	Val Asn Lys Leu Ile
Gln Ile Lys Ser Ser Asp Glu Arg Asn Thr	365	370	Leu Met Ala Gly Leu
Pro Thr Tyr Pro Leu Gly Gly Thr Ser Ile	380	385	390
Tyr Ala Phe Gln Val Ile Gly Glu Leu His	395	400	Ser Gln Leu Asp Gly
Ser Glu Val Leu Leu Leu Thr Asp Gly Glu	410	415	Asp Asn Thr Ala Ser
Ser Cys Ile Asp Glu Val Lys Gln Ser Gly	425	430	435
Ile Ala Leu Gly Arg Ala Ala Asp Glu Ala	440	445	Val Ile Glu Met Ser
Lys Ile Thr Gly Gly Ser His Phe Tyr Val	455	460	465
Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala	470	475	Leu Thr Ser Gly Asn
Thr Asp Leu Ser Gln Lys Ser Leu Gln Leu	485	490	495
Thr Leu Asn Ser Asn Ala Trp Met Asn Asp	500	505	Thr Val Ile Ile Asp
Ser Thr Val Gly Lys Asp Thr Phe Leu Ile	515	520	Thr Trp Asn Ser
Leu Pro Pro Ser Ile Ser Leu Trp Asp Pro	530	535	Ser Gly Thr Ile Met
Glu Asn Phe Thr Val Asp Ala Thr Ser Lys	545	550	Met Tyr Leu Ser
Ile Pro Gly Thr Ala Lys Val Gly Thr Trp	560	565	555
Ala Lys Ala Asn Pro Glu Thr Leu Thr Ile	575	580	Thr Val Thr Ser Arg
Ala Ala Asn Ser Ser Val Pro Pro Ile Thr			585
Ala Thr Val Asn Ala Lys Met			

590	595	600
Asn Lys Asp Val Asn Ser Phe Pro Ser Pro Met Ile Val Tyr Ala		
605	610	615
Glu Ile Leu Gln Gly Tyr Val Pro Val Leu Gly Ala Asn Val Thr		
620	625	630
Ala Phe Ile Glu Ser Gln Asn Gly His Thr Glu Val Leu Glu Leu		
635	640	645
Leu Asp Asn Gly Ala Gly Ala Asp Ser Phe Lys Asn Asp Gly Val		
650	655	660
Tyr Ser Arg Tyr Phe Thr Ala Tyr Thr Glu Asn Gly Arg Tyr Ser		
665	670	675
Leu Lys Val Arg Ala His Gly Gly Ala Asn Thr Ala Arg Leu Lys		
680	685	690
Leu Arg Pro Pro Leu Asn Arg Ala Ala Tyr Ile Pro Gly Trp Val		
695	700	705
Val Asn Gly Glu Ile Glu Ala Asn Pro Pro Arg Pro Glu Ile Asp		
710	715	720
Glu Asp Thr Gln Thr Thr Leu Glu Asp Phe Ser Arg Thr Ala Ser		
725	730	735
Gly Gly Ala Phe Val Val Ser Gln Val Pro Ser Leu Pro Leu Pro		
740	745	750
Asp Gln Tyr Pro Pro Ser Gln Ile Thr Asp Leu Asp Ala Thr Val		
755	760	765
His Glu Asp Lys Ile Ile Leu Thr Trp Thr Ala Pro Gly Asp Asn		
770	775	780
Phe Asp Val Gly Lys Val Gln Arg Tyr Ile Ile Arg Ile Ser Ala		
785	790	795
Ser Ile Leu Asp Leu Arg Asp Ser Phe Asp Asp Ala Leu Gln Val		
800	805	810
Asn Thr Thr Asp Leu Ser Pro Lys Glu Ala Asn Ser Lys Glu Ser		
815	820	825
Phe Ala Phe Lys Pro Glu Asn Ile Ser Glu Glu Asn Ala Thr His		
830	835	840
Ile Phe Ile Ala Ile Lys Ser Ile Asp Lys Ser Asn Leu Thr Ser		
845	850	855
Lys Val Ser Asn Ile Ala Gln Val Thr Leu Phe Ile Pro Gln Ala		
860	865	870
Asn Pro Asp Asp Ile Asp Pro Thr Pro Thr Pro Thr Pro Thr Pro		
875	880	885
Thr Pro Asp Lys Ser His Asn Ser Gly Val Asn Ile Ser Thr Leu		
890	895	900
Val Leu Ser Val Ile Gly Ser Val Val Ile Val Asn Phe Ile Leu		

905

910

915

Ser Thr Thr Ile

<210> 380
<211> 3877
<212> DNA
<213> Homo sapiens

<400> 380
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gaccaggagg agcaatgtat tagccaccc ctaacccctt cttcttgaac 200
ccccagttat gccaggattt actagagagt gtcaactcaa ccagcaagcg 250
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cccaggccgc ctttccgttgc ttctgttgc cgcagggtggaa caaggccatgc 1050
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tagtgggtttact ctacagaagg tggatgttgc ggttgcgttgc ctttccgttgc 1150
accccgaggaa gaaggcctgttgc aggaaggaca agcggggatgc gttgggtggaa 1200
gccattgaat cagccttgc gaccctgttgc aatccgttgc agaacagcccc 1250
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<210> 381
<211> 532
<212> PRT
<213> *Homo sapiens*

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<400> 381
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      20          25                  30
Met Leu Ala Cys Thr Pro Lys Gly Asp Glu Glu Gln Leu Ala Leu
      35          40                  45
Pro Arg Ala Asn Ser Pro Thr Gly Lys Glu Gly Tyr Gln Ala Val
      50          55                  60
Leu Gln Glu Trp Glu Glu Gln His Arg Asn Tyr Val Ser Ser Leu
      65          70                  75
Lys Arg Gln Ile Ala Gln Leu Lys Glu Glu Leu Gln Glu Arg Ser
      80          85                  90

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Glu Gln Leu Arg Asn Gly Gln Tyr Gln Ala Ser Asp Ala Ala Gly
 95 100 105
 Leu Gly Leu Asp Arg Ser Pro Pro Glu Lys Thr Gln Ala Asp Leu
 110 115 120
 Leu Ala Phe Leu His Ser Gln Val Asp Lys Ala Glu Val Asn Ala
 125 130 135
 Gly Val Lys Leu Ala Thr Glu Tyr Ala Ala Val Pro Phe Asp Ser
 140 145 150
 Phe Thr Leu Gln Lys Val Tyr Gln Leu Glu Thr Gly Leu Thr Arg
 155 160 165
 His Pro Glu Glu Lys Pro Val Arg Lys Asp Lys Arg Asp Glu Leu
 170 175 180
 Val Glu Ala Ile Glu Ser Ala Leu Glu Thr Leu Asn Asn Pro Ala
 185 190 195
 Glu Asn Ser Pro Asn His Arg Pro Tyr Thr Ala Ser Asp Phe Ile
 200 205 210
 Glu Gly Ile Tyr Arg Thr Glu Arg Asp Lys Gly Thr Leu Tyr Glu
 215 220 225
 Leu Thr Phe Lys Gly Asp His Lys His Glu Phe Lys Arg Leu Ile
 230 235 240
 Leu Phe Arg Pro Phe Ser Pro Ile Met Lys Val Lys Asn Glu Lys
 245 250 255
 Leu Asn Met Ala Asn Thr Leu Ile Asn Val Ile Val Pro Leu Ala
 260 265 270
 Lys Arg Val Asp Lys Phe Arg Gln Phe Met Gln Asn Phe Arg Glu
 275 280 285
 Met Cys Ile Glu Gln Asp Gly Arg Val His Leu Thr Val Val Tyr
 290 295 300
 Phe Gly Lys Glu Glu Ile Asn Glu Val Lys Gly Ile Leu Glu Asn
 305 310 315
 Thr Ser Lys Ala Ala Asn Phe Arg Asn Phe Thr Phe Ile Gln Leu
 320 325 330
 Asn Gly Glu Phe Ser Arg Gly Lys Gly Leu Asp Val Gly Ala Arg
 335 340 345
 Phe Trp Lys Gly Ser Asn Val Leu Leu Phe Phe Cys Asp Val Asp
 350 355 360
 Ile Tyr Phe Thr Ser Glu Phe Leu Asn Thr Cys Arg Leu Asn Thr
 365 370 375
 Gln Pro Gly Lys Lys Val Phe Tyr Pro Val Leu Phe Ser Gln Tyr
 380 385 390
 Asn Pro Gly Ile Ile Tyr Gly His His Asp Ala Val Pro Pro Leu
 395 400 405

Glu Gln Gln Leu Val Ile Lys Lys Glu Thr Gly Phe Trp Arg Asp
410 415 420

Phe Gly Phe Gly Met Thr Cys Gln Tyr Arg Ser Asp Phe Ile Asn
425 430 435

Ile Gly Gly Phe Asp Leu Asp Ile Lys Gly Trp Gly Gly Glu Asp
440 445 450

Val His Leu Tyr Arg Lys Tyr Leu His Ser Asn Leu Ile Val Val
455 460 465

Arg Thr Pro Val Arg Gly Leu Phe His Leu Trp His Glu Lys Arg
470 475 480

Cys Met Asp Glu Leu Thr Pro Glu Gln Tyr Lys Met Cys Met Gln
485 490 495

Ser Lys Ala Met Asn Glu Ala Ser His Gly Gln Leu Gly Met Leu
500 505 510

Val Phe Arg His Glu Ile Glu Ala His Leu Arg Lys Gln Lys Gln
515 520 525

Lys Thr Ser Ser Lys Lys Thr
530

<210> 382

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 382

ctcggggaaa gggacttgat gttgg 25

<210> 383

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 383

gcgaaggtaa gcctctatct cgtgcc 26

<210> 384

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 384

cagcc tacac gtattgagg 19

<210> 385

<211> 48

<212> DNA

gttgaccatt tctacaattt gtaaaagtcc aatctgtgct aacttaataa 1300
agaataatac atctctttt aaaaaaaaaa aaaaaaaaaa aaaaaaa 1346

<210> 387
<211> 212
<212> PRT
<213> Homo sapiens

<400> 387
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1 5 10 15
Leu Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser
20 25 30
Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn
35 40 45
Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys
50 55 60
Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys
65 70 75
Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr Asp Pro
80 85 90
Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala Ile
95 100 105
Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp
110 115 120
Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro
125 130 135
Met Asp Pro Ser Val Pro Ile Trp Ile Ile Phe Gly Val Ile
140 145 150
Phe Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly
155 160 165
Ile Trp Gln Arg Arg Lys Asn Lys Glu Pro Ser Glu Val Asp
170 175 180
Asp Ala Glu Asp Lys Cys Glu Asn Met Ile Thr Ile Glu Asn Gly
185 190 195
Ile Pro Ser Asp Pro Leu Asp Met Lys Gly Gly Ile Leu Met Met
200 205 210
Pro Ser

<210> 388
<211> 1371
<212> DNA
<213> Homo sapiens

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 gaaatttat acctccggg tgctggaggc tgtaatggg acagatgctc 250
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 gtgacctgga attttcgcc tctagacggg ggacctgago agtttgatt 350
 ctactaccac atagatccct tccaaaccat gagtggccgg tttaggacc 400
 gggtgttgc ggatggaaat cctgagcggt acgatgctc catcttctc 450
 tggaaactgc agttcgacga caatggaca tacacctgccc aggtgaagaa 500
 cccacactgat gttgatgggg tgataggga gatccggc acgctcggtc 550
 acactgtacg cttctctgag atccacttcc tggctctggc cattggctct 600
 gcctgtgcac tgatgatcat aatagaatt gtatggtcc tcttcagca 650
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 aataaaaaga agaggaaagg ctcaccaag agaaaaaggt ctctgtttat 750
 tttagaagaca cagactaaca attttagatg gaagctgaga tgattccaa 800
 gaacaagaac ccttagtattt cttgaagttt atggaaacctt ttcttggct 850
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 acagtaaaatc ctaaattcaa actgttaaat gacatttttata tttttatgtc 1300
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<210> 389

<211> 215

<212> PRT

<213> Homo sapiens

<400> 389

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Ile Gln Leu Thr Ala Leu Trp Pro Ile Ala Ala Val Glu Ile Tyr
20 25 30

Thr Ser Arg Val Leu Glu Ala Val Asn Gly Thr Asp Ala Arg Leu
35 40 45

Lys Cys Thr Phe Ser Ser Phe Ala Pro Val Gly Asp Ala Leu Thr
50 55 60

Val Thr Trp Asn Phe Arg Pro Leu Asp Gly Gly Pro Glu Gln Phe
65 70 75

Val Phe Tyr Tyr His Ile Asp Pro Phe Gln Pro Met Ser Gly Arg
80 85 90

Phe Lys Asp Arg Val Ser Trp Asp Gly Asn Pro Glu Arg Tyr Asp
95 100 105

Ala Ser Ile Leu Leu Trp Lys Leu Gln Phe Asp Asp Asn Gly Thr
110 115 120

Tyr Thr Cys Gln Val Lys Asn Pro Pro Asp Val Asp Gly Val Ile
125 130 135

Gly Glu Ile Arg Leu Ser Val Val His Thr Val Arg Phe Ser Glu
140 145 150

Ile His Phe Leu Ala Leu Ala Ile Gly Ser Ala Cys Ala Leu Met
155 160 165

Ile Ile Ile Val Ile Val Val Leu Phe Gln His Tyr Arg Lys
170 175 180

Lys Arg Trp Ala Glu Arg Ala His Lys Val Val Glu Ile Lys Ser
185 190 195

Lys Glu Glu Glu Arg Leu Asn Gln Glu Lys Lys Val Ser Val Tyr
200 205 210

Leu Glu Asp Thr Asp
215

<210> 390

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 390

ccgaggccat ctagaggcca gagc 24

<210> 391

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

acaggcagag ccaatggcca gagc 24

<210> 392
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 392
gaggaggactg cgggagtttg ggaccttgt gcagacgtgc tcatg 45

<210> 393
<211> 471
<212> DNA
<213> Homo sapiens

<400> 393
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atccgacaac agctgctcca gctgacacgt atccagctac tggtcctgt 150
gatgatgaag cccctgtatgc taaaaccact gctgctgcaa ccactgcac 200
caactgctgtc cttaccactg caaccacccg tgcttctacc actgctcgta 250
aagacattcc agttttacc aatggggtt gggatctccc gaatggtaga 300
gtgtgtccct gagatggaaat cagcttgagt cttctgcaat tggtcacaac 350
tattcatgtc ttctgtgatt tcatccaact acttacccctt cctacgatat 400
cccccttatac tctaatacgat ttattttctt tcaaataaaaaa aataactatg 450
agcaacataaa aaaaaaaaaa a 471

<210> 394
<211> 90
<212> PRT
<213> Homo sapiens

<400> 394
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Leu Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr
20 25 30
Tyr Pro Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu
35 40 45
Thr Thr Ala Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr
50 55 60
Ala Thr Thr Ala Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val
65 70 75
Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
80 85 90

<210> 395
<211> 25

卷之三

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 395
gctccctgtat cttcatgtca ccacc 25

<210> 396
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 396
caggcacaca ctctaccatt cgggag 26

<210> 397
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 397
ccatcttctt ggtctctgcg cagaatccga caacagctgc tc 42

<210> 398
<211> 907
<212> DNA
<213> Homo sapiens

<400> 398
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aaccttggac cccttaggggt ctggatttgc tggtaacaa gataacctga 100
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gtttcacgg tggctctggc cttcccttgcg gagagagtgt cttgggtcag 200
ggacgcagag gacgctcaca gactccagcc ctttggattacc gagaggacac 250
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aaatttagcca ggcacagtgg tgtcactgg tagtcccaagt tactcgggag 800
gctgaggcgac gaaaatcgct tgaaccagg aggccgacgt tgccgtgagc 850
cgagatcgcg ccgcgtgatc cagccctgggc gacaagagtg agactccatc 900
tcacaca 907

<210> 399
<211> 120
<212> PRT
<213> Homo sapiens

<400> 399
Met Leu Pro Pro Ala Leu Pro Pro Ala Leu Val Phe Thr Val Ala
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Trp Ser Leu Leu Ala Glu Arg Val Ser Trp Val Arg Asp Ala Glu
20 25 30
Asp Ala His Arg Leu Gln Pro Phe Val Thr Glu Arg Thr Leu Gly
35 40 45
Lys Val Gln Arg Trp Ser Gly Val His Thr Gln Thr Gly Gly Arg
50 55 60
Ala Gly Gly Gln Phe Cys Cys Ala Trp Leu Asp Ser Lys Arg
65 70 75
Val Leu Ala Ser Pro Gly Trp Gly Ala Ala Asn Ser Ile Lys Asn
80 85 90
Gln Arg Val Trp Ala Pro Ala Thr Glu Ser Ser Ala Gln Leu Leu
95 100 105
Cys Cys Trp Pro Val Gly Val Ala Arg Gly Gly Ala Leu Cys Gln
110 115 120

<210> 400
<211> 893
<212> DNA
<213> Homo sapiens

<400> 400
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ccggccctgg tcagcggccc ccatgggggg cccagaactg gcacagcatg 100
aggagctgac cctgtcttc catgggaccc tgcaacctgg ccaggccctc 150
aacgggtgt acaggaccac ggagggacgg ctgacaaaagg ccaggaacag 200
cctgggtctc tatggccca caatagaact cctggggcag gaggtcagcc 250
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tagaagtcca gctgaggagc gcctggctgg gccctgccta ccgagaattt 450
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cacaggccac gtgcagcggc agaggcggga gatggtgca cagcagcatc 550
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cgccccgtga ggccccgtg cagggaggag ctgcctgttc actggatca 700
gccagggcgc cgggccccac ttctgagcac agagcagaga cagacgcagg 750
cggggacaaa ggcagaggat gtagcccat tggggagggg tggaggaagg 800
acatgtaccc tttcatgcct acacacccct cattaaagca gagtcgtggc 850
atttcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 893

<210> 401
<211> 198
<212> PRT
<213> Homo sapiens

<400> 401
Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val
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Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu
35 40 45
Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg Leu
50 55 60
Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu
65 70 75
Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu
80 85 90
Leu Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu
95 100 105
Gln Leu Gln Ala Glu Ala Thr Ala Glu Val Leu Gly Glu Val Ala
110 115 120
Gln Ala Gln Lys Val Leu Arg Asp Ser Val Gln Arg Leu Glu Val
125 130 135
Gln Leu Arg Ser Ala Trp Leu Gly Pro Ala Tyr Arg Glu Phe Glu
140 145 150
Val Leu Lys Ala His Ala Asp Lys Gln Ser His Ile Leu Trp Ala
155 160 165
Leu Thr Gly His Val Gln Arg Gln Arg Arg Glu Met Val Ala Gln
170 175 180
Gln His Arg Leu Arg Gln Ile Gln Glu Arg Leu His Thr Ala Ala

185

190

195

Leu Pro Ala

<210> 402
<211> 1915
<212> DNA
<213> *Homo sapiens*

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gagattgaga gtggacttac attccctttt ttacattttc gtatatttat 1500
tttttttagc catcattata tgtttaagtc tattatggc aaccaatctt 1550
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cttcaaataa atatgttta aacattgaat gtgttttg aacaatatcc 1800
cactttgc aactttaacta cacatgttg gaattaagtt ttagctgtt 1850
tcatttgctca ataataaaagc ctgaattctg atcaataaaaa aaaaaaaaaa 1900
aaaaaaaaaa aaaaa 1915

<210> 403

<211> 206

<212> PRT

<213> Homo sapiens

<400> 403

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Val	Ile	Cys	Ile	Leu	Val	Ile	Thr	Leu	Leu	Leu	Asp	Gln	Thr	Thr
					20				25					30
Ser	His	Thr	Ser	Arg	Leu	Lys	Ala	Arg	Lys	His	Ser	Lys	Arg	Arg
				35				40						45
Val	Arg	Asp	Lys	Asp	Gly	Asp	Leu	Lys	Thr	Gln	Ile	Glu	Lys	Leu
				50				55						60
Trp	Thr	Glu	Val	Asn	Ala	Leu	Lys	Glu	Ile	Gln	Ala	Leu	Gln	Thr
				65				70						75
Val	Cys	Leu	Arg	Gly	Thr	Lys	Val	His	Lys	Lys	Cys	Tyr	Leu	Ala
				80				85						90
Ser	Glu	Gly	Leu	Lys	His	Phe	His	Glu	Ala	Asn	Glu	Asp	Cys	Ile
				95				100						105
Ser	Lys	Gly	Gly	Ile	Leu	Val	Ile	Pro	Arg	Asn	Ser	Asp	Glu	Ile
				110				115						120
Asn	Ala	Leu	Gln	Asp	Tyr	Gly	Lys	Arg	Ser	Leu	Pro	Gly	Val	Asn
				125				130						135
Asp	Phe	Trp	Leu	Gly	Ile	Asn	Asp	Met	Val	Thr	Glu	Gly	Lys	Phe
				140				145						150
Val	Asp	Val	Asn	Gly	Ile	Ala	Ile	Ser	Phe	Leu	Asn	Trp	Asp	Arg

155	160	165
Ala Gln Pro Asn Gly Gly Lys Arg Glu Asn Cys Val Leu Phe Ser 170	175	180
Gln Ser Ala Gln Gly Lys Trp Ser Asp Glu Ala Cys Arg Ser Ser 185	190	195
Lys Arg Tyr Ile Cys Glu Phe Thr Ile Pro Lys 200	205	

<210> 404
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 404
cctggttatc cccaggaact ccgac 25

<210> 405
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 405
ctcttgctgc tgcgacaggc ctc 23

<210> 406
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 406
cgccctcaa gactatggta aaaggagcct gccaggtgtc aatgac 46

<210> 407
<211> 570
<212> DNA
<213> Homo sapiens

<400> 407
gcgaggaccg ggtataagaa gcctcggtgc cttgccccgg cagccgcagg 50
ttccccggcc gccccggaccc ccccgcccat gaagctcgcc gcctccctgg 100
ggctctggcg tggccctgtcc tgcagctccg ctgctgtt ctttagtgggc 150
tcggccaagc ctgtggccca gcctgtcgct gcgcgtggagt cggccggcgg 200
ggccggggcc gggaccctgg ccaaccctt cggcacccctc aaccggctga 250
agctccgt gaggcagcgtc ggcatccccc tgaaccacct catagaggc 300
tcccagaagt gtgtggctga gctgggtccc caggccgtgg gggccgtgaa 350

THEORY AND METHODS

ggccctgaag gccctgtgg gggccctgac agtgtttggc tgagccgaga 400
ctggagcatc tacacctgag gacaagacgc tgcccacccg cgaggggctga 450
aaaccccgcc gcggggagga ccttcccccg gcccctctca 500
ataaacgtgg ttaagagcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 550
aaaaaaaaa aaaaaaaaaa 570

<210> 408
<211> 104
<212> PRT
<213> Homo sapiens

<400> 408
Met Lys Leu Ala Ala Leu Leu Gly Leu Cys Val Ala Leu Ser Cys
1 5 10 15
Ser Ser Ala Ala Ala Phe Leu Val Gly Ser Ala Lys Pro Val Ala
20 25 30
Gln Pro Val Ala Ala Leu Glu Ser Ala Ala Glu Ala Gly Ala Gly
35 40 45
Thr Leu Ala Asn Pro Leu Gly Thr Leu Asn Pro Leu Lys Leu Leu
50 55 60
Leu Ser Ser Leu Gly Ile Pro Val Asn His Leu Ile Glu Gly Ser
65 70 75
Gln Lys Cys Val Ala Glu Leu Gly Pro Gln Ala Val Gly Ala Val
80 85 90
Lys Ala Leu Lys Ala Leu Leu Gly Ala Leu Thr Val Phe Gly
95 100

<210> 409
<211> 2089
<212> DNA
<213> Homo sapiens

<400> 409
tgaaggactt ttccaggacc caaggccaca cactggaagt ctgcagctg 50
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ggccccccact cctcagtcgc cagagacccc agcccccctcg aaccagacca 200
gcagggttagt gcaggctccc agggaggaa aggaagatga gcaggaggcc 250
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tgtatgtcaaa gagactttt tcaatttatac caagaggat tttgatacag 650
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aatcattaca ttaacaaaga gactcgaaaaaaaattccca aactgtttga 750
tgtagattaat cctgaaacca aattaattct tttggattac atcttggatca 800
aaggaaatg gttgacccca tttgaccctg ttttcaccga agtcgacact 850
ttccacactgg acaagttacaa gaccattha gttccccatga tgtaacggtgc 900
aggcaagttt gcctccacctt ttgacaagaa tttttgttgc catgtcctca 950
aactggcccta ccaaggaaat gccaccatgc ttgggttctt catggagaaa 1000
atgggtgacc acctcgccct tgaagactac ctgaccacag acttgggtga 1050
gacatggctc agaaacatga aaaccagaaa catggagtt ttcttccga 1100
agttaagct agatcagaag tatgagatgc atgagctgt taggcagatg 1150
ggaatcagaa gaatcttctc accctttgtt gaccttagtg aactctcagc 1200
tactgaaaga aatctccaag tatccagggt tttacgaaga acagtgttt 1250
aagttgatga aaggggactt gggcagtgg caggaatctt gtcagaaattt 1300
actgcttattt ccattgcctcc ttttcatcaaa gtggaccggc cattttctt 1350
catgatctat gaagaaacctt ctgaaatgtc tttttttttt ggcagggtgg 1400
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aagtactca tgggcggagaa gcatagacag tttggagaca ttggcaagg 1850
ggagaatttca catcctgggtt gggcagacggc aggacgtgc aagattccat 1900
cccactactc agaatggcat gctgcttaag actttttagat tttttttttt 1950
tggaaatttt catttaatgtt ttttggacca tgggttgcacca tggtaactg 2000
agactgcaga aagcaaaacc atggataagg gaggactact acaaaaagcat 2050
taaattgtata catatttttt aaaaaaaaaaaaaaaa 2089

<210> 410
<211> 444
<212> PRT
<213> Homo sapiens

<400> 410
Met Lys Val Val Pro Ser Leu Leu Leu Ser Val Leu Leu Ala Gln
1 5 10 15
Val Trp Leu Val Pro Gly Leu Ala Pro Ser Pro Gln Ser Pro Glu
20 25 30
Thr Pro Ala Pro Gln Asn Gln Thr Ser Arg Val Val Gln Ala Pro
35 40 45
Arg Glu Glu Glu Glu Asp Glu Gln Glu Ala Ser Glu Glu Lys Ala
50 55 60
Gly Glu Glu Glu Lys Ala Trp Leu Met Ala Ser Arg Gln Gln Leu
65 70 75
Ala Lys Glu Thr Ser Asn Phe Gly Phe Ser Leu Leu Arg Lys Ile
80 85 90
Ser Met Arg His Asp Gly Asn Met Val Phe Ser Pro Phe Gly Met
95 100 105
Ser Leu Ala Met Thr Gly Leu Met Leu Gly Ala Thr Gly Pro Thr
110 115 120
Glu Thr Gln Ile Lys Arg Gly Leu His Leu Gln Ala Leu Lys Pro
125 130 135
Thr Lys Pro Gly Leu Leu Pro Ser Leu Phe Lys Gly Leu Arg Glu
140 145 150
Thr Leu Ser Arg Asn Leu Glu Leu Gly Leu Ser Gln Gly Ser Phe
155 160 165
Ala Phe Ile His Lys Asp Phe Asp Val Lys Glu Thr Phe Phe Asn
170 175 180
Leu Ser Lys Arg Tyr Phe Asp Thr Glu Cys Val Pro Met Asn Phe
185 190 195
Arg Asn Ala Ser Gln Ala Lys Arg Leu Met Asn His Tyr Ile Asn
200 205 210
Lys Glu Thr Arg Gly Lys Ile Pro Lys Leu Phe Asp Glu Ile Asn
215 220 225
Pro Glu Thr Lys Leu Ile Leu Val Asp Tyr Ile Leu Phe Lys Gly
230 235 240
Lys Trp Leu Thr Pro Phe Asp Pro Val Phe Thr Glu Val Asp Thr
245 250 255
Phe His Leu Asp Lys Tyr Lys Thr Ile Lys Val Pro Met Met Tyr
260 265 270
Gly Ala Gly Lys Phe Ala Ser Thr Phe Asp Lys Asn Phe Arg Cys
275 280 285

His Val Leu Lys Leu Pro Tyr Gln Gly Asn Ala Thr Met Leu Val
290 295 300

Val Leu Met Glu Lys Met Gly Asp His Leu Ala Leu Glu Asp Tyr
305 310 315

Leu Thr Thr Asp Leu Val Glu Thr Trp Leu Arg Asn Met Lys Thr
320 325 330

Arg Asn Met Glu Val Phe Phe Pro Lys Phe Lys Leu Asp Gln Lys
335 340 345

Tyr Glu Met His Glu Leu Leu Arg Gln Met Gly Ile Arg Arg Ile
350 355 360

Phe Ser Pro Phe Ala Asp Leu Ser Glu Leu Ser Ala Thr Gly Arg
365 370 375

Asn Leu Gln Val Ser Arg Val Leu Arg Arg Thr Val Ile Glu Val
380 385 390

Asp Glu Arg Gly Thr Glu Ala Val Ala Gly Ile Leu Ser Glu Ile
395 400 405

Thr Ala Tyr Ser Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe
410 415 420

His Phe Met Ile Tyr Glu Glu Thr Ser Gly Met Leu Leu Phe Leu
425 430 435

Gly Arg Val Val Asn Pro Thr Leu Leu
440

<210> 411

<211> 636

<212> DNA

<213> Homo sapiens

<400> 411
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tgtggggaggc aggtgcagtc ccagcaccca aggtcccttat caagatgcaa 150
gtcaaaacact ggcctcaga gcaggaccca gagaaggccct ggggcgcccg 200
tgtggtgaggc cttccggaga aggacgacca gctggtggtg ctgttccctg 250
tccagaagcc gaaactcttg accaccgagg agaagccacg aggtcaggc 300
agggggccca tccttccagg caccaaggcc tggatggaga ccgaggacac 350
cctggggccgt gtccctgagtc ccgagcccgaa ccatgacacg ctgttaccacc 400
ctccgcctga ggaggaccag ggcgaggaga ggccccgggt gtgggtgatg 450
ccaaatcacc aggtgctccctt gggaccggag gaagaccaag accacatcta 500
ccaccccccag tagggctcca gggccatca ctggcccccgc cctgtcccaa 550
ggccccaggt gttgggactg ggaccctccc taccctgccc cagcttagaca 600

aataaaccggc agcaggcaaa aaaaaaaaaa aaaaaa 636

<210> 412
<211> 151
<212> PRT
<213> Homo sapiens

<400> 412
Met Arg Arg Leu Leu Leu Val Thr Ser Leu Val Val Val Leu Leu
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Trp Glu Ala Gly Ala Val Pro Ala Pro Lys Val Pro Ile Lys Met
20 25 30
Gln Val Lys His Trp Pro Ser Glu Gln Asp Pro Glu Lys Ala Trp
35 40 45
Gly Ala Arg Val Val Glu Pro Pro Glu Lys Asp Asp Gln Leu Val
50 55 60
Val Leu Phe Pro Val Gln Lys Pro Lys Leu Leu Thr Thr Glu Glu
65 70 75
Lys Pro Arg Gly Gln Gly Arg Gly Pro Ile Leu Pro Gly Thr Lys
80 85 90
Ala Trp Met Glu Thr Glu Asp Thr Leu Gly Arg Val Leu Ser Pro
95 100 105
Glu Pro Asp His Asp Ser Leu Tyr His Pro Pro Pro Glu Glu Asp
110 115 120
Gln Gly Glu Glu Arg Pro Arg Leu Trp Val Met Pro Asn His Gln
125 130 135
Val Leu Leu Gly Pro Glu Glu Asp Gln Asp His Ile Tyr His Pro
140 145 150

Gln

<210> 413
<211> 1176
<212> DNA
<213> Homo sapiens

<400> 413
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aggagctctc tgcacccaag gaaagtgcag ctgagactca gacaagattta 100
caatgaacca actcagcttc ctgcgtttc tcatacgccac caccagagga 150
tggagttacag atgaggctaa tacttacttc aaggaatgg cctgttcttc 200
gtctccatctc ctgcccagaa gctgcaagga aatcaaagac gaatgtccta 250
gtgcatttga tggcctgtat ttctccgcac ctgagaatgg tgttatctac 300
cagaccttc gtgacatgc ctctgggggtt ggccggctggaa ccctgggtggc 350
cagcgtgcat gagaatgaca tgcgtggaa gtgcacgggtt ggcgatcgct 400

ggtccagtca gcagggcagc aaagcagact acccagaggg ggacggcaac 450
 tgggcaact acaacacctt tggatctgc gaggcgcca cgagcgatga 500
 ctacaagaac cctggctact acgacatcca ggccaaggac ctgggcatt 550
 ggcacgtgcc caataagtcc cccatgcagc actggagaaa cagctccctg 600
 ctgaggtacc gcacggcac tggcttcctc cagacactgg gacataatct 650
 gtttggcatc taccagaaat atccagtcaa atatggagaa ggaaaagtgtt 700
 ggactgacaa cggcccccgtg atccctgtgg tctatgattt tgccgacgcc 750
 cagaaaaacag catcttatta ctacacctat ggccagcggg aattcactgc 800
 gggatttgtt cagttcaggg tatataaa cgagagagca gccaacgcct 850
 tgtgtgttgtt aatgagggtc accggatgt aacttgacca tcactgcatt 900
 ggtggaggag gatactttcc agaggccagt ccccagcgt gtggagattt 950
 ttctgggttt gattggagt gatatggaac tcatgttgtt tacagcagca 1000
 gccgtgagat aactgaggca gctgtgttc tattctatcg ttgagagttt 1050
 tttggggagg aaccctcacc tctccctccca accatgagat cccaaggatg 1100
 gagaacaact tacccagtag ctagaatgtt aatggcagaa gagaaaacaa 1150
 taaaatcatat tgactcaaga aaaaaa 1176

<210> 414
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 414
 Met Asn Gln Leu Ser Phe Leu Leu Phe Ile Ala Thr Thr Arg
 1 5 10 15
 Gly Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr
 20 25 30
 Cys Ser Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys
 35 40 45
 Asp Glu Cys Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr
 50 55 60
 Glu Asn Gly Val Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly
 65 70 75
 Gly Gly Gly Trp Thr Leu Val Ala Ser Val His Glu Asn Asp Met
 80 85 90
 Arg Gly Lys Cys Thr Val Gly Asp Arg Trp Ser Ser Gln Gln Gly
 95 100 105
 Ser Lys Ala Asp Tyr Pro Glu Gly Asp Gly Asn Trp Ala Asn Tyr
 110 115 120
 Asn Thr Phe Gly Ser Ala Glu Ala Ala Thr Ser Asp Asp Tyr Lys

	125		130		135
Asn Pro Gly Tyr	Tyr Asp Ile Gln Ala	Lys Asp Leu Gly Ile	Trp		
140		145		150	
His Val Pro Asn Lys Ser Pro Met Gln	His Trp Arg Asn Ser	Ser			
155		160		165	
Leu Leu Arg Tyr Arg Thr Asp Thr Gly	Phe Leu Gln Thr Leu	Gly			
170		175		180	
His Asn Leu Phe Gly Ile Tyr Gln Lys	Tyr Pro Val Lys Tyr	Gly			
185		190		195	
Glu Gly Lys Cys Trp Thr Asp Asn Gly	Pro Val Ile Pro Val	Val			
200		205		210	
Tyr Asp Phe Gly Asp Ala Gln Lys Thr	Ala Ser Tyr Tyr Ser	Pro			
215		220		225	
Tyr Gly Gln Arg Glu Phe Thr Ala Gly	Phe Val Gln Phe Arg	Val			
230		235		240	
Phe Asn Asn Glu Arg Ala Ala Asn Ala	Leu Cys Ala Gly Met	Arg			
245		250		255	
Val Thr Gly Cys Asn Thr Glu His His	Cys Ile Gly Gly Gly	Gly			
260		265		270	
Tyr Phe Pro Glu Ala Ser Pro Gln Gln	Cys Gly Asp Phe Ser	Gly			
275		280		285	
Phe Asp Trp Ser Gly Tyr Gly Thr His	Val Gly Tyr Ser Ser	Ser			
290		295		300	
Arg Glu Ile Thr Glu Ala Ala Val Leu	Leu Phe Tyr Arg				
305		310			

<210> 415
<211> 1281
<212> DNA
<213> *Homo sapiens*

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<400> 415  
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cgcgctggag cccacgaggc tgccgcatcc tgcctcgga acaatggac 100  
tcggcgccgc aggtgcttgg gcccgcgtgc tcctggggac gtcgcaggta 150  
ctagcgtgc tggggccgc ccatgaaagc gcagccatgg cggcatctgc 200  
aaacatagag aattctggc ttccacacaa ctccaggatct aactcaacag 250  
agactctcca acatgtgcct tctgaccata caaatgaaac ttccaaacagt 300  
actgtgaac caccacacttc agttgcctca gactccagta atacaacagg 350  
caccacccatg aaacacctacag cgccatctaa tacaacaaca ccaggatgg 400  
tctcaacaaa tatgacttct accaccttaa agtctacacc caaaacaaca 450  
agtgtttcac aqaacacatc tcagatatca acatccacaa tgaccgttaa 500
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ccacaatagt tcagtgacat ctgctgttc atcagtaaca atcacaacaa 550
ctatgcattc tgaagcaaag aaaggatcaa aatttgatac tgggagctt 600
gttgggtgta ttgttattaac gctgggagtt ttatctattc tttacattgg 650
atgcaaaatg tattactcaa gaagaggcat tcggtatcg accatagatg 700
aacatgatgc catcattaa ggaatccat ggaccaagga tggatacacag 750
attgatgctg ccctatcaat taattttgtt ttatataatag tttaaaacaa 800
tattcttctt ttgaaaatag tataaacagg ccatgcatat aatgtacagt 850
gttattacgt aatatgtaaa gattctcaa ggttaacaagg gtttgggtt 900
tgaataaaac atctggatct tatagaccgt tcatacaatg gtttttagcaa 950
gttcatagta agacaaacaa gtcctatctt tttttttgg ctgggggtgg 1000
ggcattggc acatatgacc agtaattgaa agacgtcatac actgaaagac 1050
agaatgccc ctgggcatac aaataagaag tttgtcacag cactcaggat 1100
tttgggtatc tttttagct cacataaga acttcagtgc ttttcagagc 1150
tggatataatc ttaattacta atgccccacaca gaaattatac aatcaaacta 1200
gatctgaaagc ataatttaag aaaaacatca acattttttg tgctttaaac 1250
tgttagtagtt ggtctagaaa caaaatactc c 1281

<210> 416

<211> 208

<212> PRT

<213> Homo sapiens

<400> 416
Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly
1 5 10 15
Thr Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala
20 25 30
Ala Met Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His
35 40 45
Asn Ser Ser Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser
50 55 60
Asp His Thr Asn Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr
65 70 75
Ser Val Ala Ser Asp Ser Ser Asn Thr Thr Val Thr Thr Met Lys
80 85 90
Pro Thr Ala Ala Ser Asn Thr Thr Pro Gly Met Val Ser Thr
95 100 105
Asn Met Thr Ser Thr Thr Leu Lys Ser Thr Pro Lys Thr Thr Ser
110 115 120
Val Ser Gln Asn Thr Ser Gln Ile Ser Thr Ser Thr Met Thr Val

125	130	135
Thr His Asn Ser Ser Val Thr Ser Ala Ala Ser Ser Val Thr Ile		
140	145	150
Thr Thr Thr Met His Ser Glu Ala Lys Lys Gly Ser Lys Phe Asp		
155	160	165
Thr Gly Ser Phe Val Gly Gly Ile Val Leu Thr Leu Gly Val Leu		
170	175	180
Ser Ile Leu Tyr Ile Gly Cys Lys Met Tyr Tyr Ser Arg Arg Gly		
185	190	195
Ile Arg Tyr Arg Thr Ile Asp Glu His Asp Ala Ile Ile		
200	205	

<210> 417
<211> 1728
<212> DNA
<213> Homo sapiens

<400> 417
cagccgggtc ccaaggctgt gcctgagcct gaggctgagc ctgagccccga 50
gcggggagcc ggtagccccggg gctccggggct gtggggaccgc tggggcccccga 100
gcgtatggcgca ccctgtgggg aggcccttctt cggcttggct ctttgcttcag 150
cctgtcggtgc ctggcgcttt ccgtgctgtc gctggcgacg ctgtcagacg 200
ccgccaagaa tttagggaggat gtcagatgtta aatgtatctg ccctccctat 250
aaagaaaatt ctggccatata ttataataag aacatatctc agaaaaggattg 300
tgattggcattt catgttgtgg agcccatgc tggcgccccggg cctgtatgttag 350
aagcatactg tctacgctgt gaatgtcaat atgaagaaag aagctctgtc 400
acaatcaagg ttaccattttt aatttatctc tccatttttgg gccttctact 450
tctgtacatg gtatatacttta ctctgggttgc gcccatactg aagaggcgcc 500
tctttggaca tgcacagtttgc atacagatgtc atgtatgtat tggggatcac 550
cagcccttttgc caaatgcaca cgatgtgtca gccccgtccc gcagtcgagc 600
caacgtgtca aacaaggtag aatatgcaca gcagcgctgg aagcttcaag 650
tccaagagac gcgaaaatgtc gtctttgacc ggcattgttg cctcagatcaa 700
ttgggaatttgc aatcaaggatgtc gacttagaaag aaacaggcgac acaactggaa 750
agaactgact ggggtttgtc ggggtttcattt ttaatacctt gttgatttca 800
ccaaactgttgc ctggaaaggatgtc caaaaactggaa agcaaaaaact tgcttgattt 850
ttttttcttg ttaacgtataat aatagagaca tttttaaaag cacacagatctc 900
aaagtcaagcc aataagtctt ttccttatttgc tgacttttac taataaaaaat 950
aatatctgcctt gtaatttttgc ttgaaggctt ttacctggaa caagcactct 1000

09918547
TEST

cttttcacc acatagttt aacttgactt tcaagataat tttcagggtt 1050
tttgttgg ttgtttttg ttgtttgtt ttggggaggg aggggaggga 1100
tgcctggaa gtggtaaca actttttca agtcactta ctaaacaaac 1150
tttgtaaat agacattacc ttctatccc gagttcatt tatattttgc 1200
agtgttagcca gcctcatcaa agagctgact tactcatttgc acctttgcac 1250
tgactgtatt atctgggtat ctgctgtgtc tgcaettcat ggttaaacggg 1300
atctaaaat cctgggtgc ttccaaaaa agcagattt cttcatgtac 1350
tgtgatgtct gatcaatgc atcctagaac aaactggcca ttgttagtt 1400
tactctaaag actaaacata gctttgggt gtgtggctt actcatcttc 1450
tagtacccctt aaggacaaat cctaaggact tggacacttg caataaagaa 1500
attttatttt aaacccaagc ctccctggat tgataatata tacacatttgc 1550
tcagcatttc cggtcggtt gagaggcagc tggttggctt ccaatatgtc 1600
cagcttggaa ctagggtctgg gggttgggtt gctcttctg aaaggctcaa 1650
ccattattgg ataactggct tttttcttcc tatgttctct ttggaatgt 1700
acaataaaaa taatttttga aacatcaa 1728

<210> 418
<211> 198
<212> PRT
<213> Homo sapiens

<400> 418
Met Ala Thr Leu Trp Gly Gly Leu Leu Arg Leu Gly Ser Leu Leu
1 5 10 15
Ser Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu
20 25 30
Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile
35 40 45
Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn
50 55 60
Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu Pro Met
65 70 75
Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu
80 85 90
Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile
95 100 105
Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Tyr Met Val
110 115 120
Tyr Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly
125 130 135

THE DIALECT OF TURKEY

Val Leu Ser

<210> 419
<211> 681
<212> DNA
<213> *Homo sapiens*

<400> 419
gcacccgtcga ccaccgtgag cagtcatggc gtactccaca gtgcagagag 50
tcgtctggc ttctgggctt gtcctggctc tgcgtcgctc gtcgtccaaag 100
gccttcttgt cccggggaa gcggcaggag cccgcgcgca cacctgaagg 150
aaaattggc cgattnccac ctatgtatca tcatacaccag gcaccccttag 200
atggccagac tccctgggctt cgtttccaga ggtctcacct tgccggaggc 250
tttgcaaagg ccaaaggata aggtggaggt gctggaggag gaggtatgtgg 300
aagaggctcg atggggcaga tatttccaat ctacggttt gggatTTTTT 350
tatataatact gtacattcta tttaaggtaa gtagaatcat ctaatactata 400
ttacatcaat gaaaatctaa tatggcgata aaaatcattt tctacattaa 450
aacttcttat agtctataaa attatttcaa atccatcata tctttaaatc 500
ctgcctcttc ttcatgaggtt acttaggata gccattttt cagtttcaca 550
taagaatgtt tactcaatgt ttaagtgttt tgccccaaaa ttccacaacta 600
acaaggcaga actaggactt gaacatggat cttttggttc ttaatccagt 650
qaqtgtataca attcaatgc a cttccctgcc a 681

<210> 420
<211> 128
<212> PRT
<213> *Homo sapiens*

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<400> 420
Met Ala Tyr Ser Thr Val Gln Arg Val Ala Leu Ala Ser Gly Leu
          5           10
          1

Val Leu Ala Leu Ser Leu Leu Leu Pro Lys Ala Phe Leu Ser Arg
          20           25
          30

Gly Lys Arg Gln Glu Pro Pro Pro Thr Pro Glu Gly Lys Leu Gly
          35           40
          45

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Arg Phe Pro Pro Met Met His His Gln Ala Pro Ser Asp Gly
50 55 60
Gln Thr Pro Gly Ala Arg Phe Gln Arg Ser His Leu Ala Glu Ala
65 70 75
Phe Ala Lys Ala Lys Gly Ser Gly Gly Ala Gly Gly Gly Gly
80 85 90
Ser Gly Arg Gly Leu Met Gly Gln Ile Ile Pro Ile Tyr Gly Phe
95 100 105
Gly Ile Phe Leu Tyr Ile Leu Tyr Ile Leu Phe Lys Val Ser Arg
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Ile Ile Leu Ile Ile Leu His Gln
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<213> Homo sapiens

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ttgaatgttt ccccgccotga gctaaccatgc catgtgggtt attcagctct 200
gatgggatgt gtttccaga gcacagaaga caaatgtata ttcaagatag 250
actggactct gtaccaggaa gagcaccgcca aggacqaata tgtgtatac 300
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cttgcgtggg gacatcttat gcaatgtatgg ctctctccctg ctccaaatgg 400
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gccccaaagag ctcattgtcc atgtgggtt attgatttagt atggatgtg 550
ttttccagag cacagaatgtt aaacacgtt ccaaggatgtt atggatattt 600
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ggagtggggat agtcagatgtt agggaaactac acctgcgttca tccacccatgg 800
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aatcgttggggat tgcattgtt gggaaattgtt tgcgttccaaat tccgttgcgtt 950
ccctgttcttgcatttgc tgaagaagac ctgtggaaat aagagttcag 1000

tgaattctac agtcttggtg aagaacacga agaagactaa tccagagata 1050
 aaagaaaaac cctgccatt tgaaagatgt gaaggggaga aacacattta 1100
 ctccccata attgtacggg aggtgatega ggaagaagaa ccaagtgaaa 1150
 aatcagaggc cacctacatg accatgcacc cagttggcc ttctctgagg 1200
 tcagatcgga acaactcaact tgaaaaaaag tcaggtgggg gaatgccaaa 1250
 acacagcaa gccttttag aagaatggag agtccttca tctcagcgc 1300
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 agactccgcg tctcccagct gtccctctgt ctcattgtt ggtcaataca 1400
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 acactggccc tggaaaccag gctgagctga gtggcctcaa acccccccgtt 1550
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<211> 394

<212> PRT

<213> Homo sapiens

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Tyr	Ser	Leu	Gly	Leu	Asn	Asp	Leu	Asn	Val	Ser	Pro	Pro	Glu	Leu
				20				25					30	
Thr	Val	His	Val	Gly	Asp	Ser	Ala	Leu	Met	Gly	Cys	Val	Phe	Gln
				35				40					45	
Ser	Thr	Glu	Asp	Lys	Cys	Ile	Phe	Lys	Ile	Asp	Trp	Thr	Leu	Ser
				50				55					60	
Pro	Gly	Glu	His	Ala	Lys	Asp	Glu	Tyr	Val	Leu	Tyr	Tyr	Tyr	Ser
				65				70					75	
Asn	Leu	Ser	Val	Pro	Ile	Gly	Arg	Phe	Gln	Asn	Arg	Val	His	Leu
				80				85					90	
Met	Gly	Asp	Ile	Leu	Cys	Asn	Asp	Gly	Ser	Leu	Leu	Gln	Asp	
				95				100					105	
Val	Gln	Glu	Ala	Asp	Gln	Gly	Thr	Tyr	Ile	Cys	Glu	Ile	Arg	Leu
				110				115					120	
Lys	Gly	Glu	Ser	Gln	Val	Phe	Lys	Ala	Val	Val	Leu	His	Val	
				125				130					135	
Leu	Pro	Glu	Glu	Pro	Lys	Glu	Leu	Met	Val	His	Val	Gly	Gly	Leu
				140				145					150	
Ile	Gln	Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Glu	Val	Lys	His	Val

TOPPS: 1996-1997

155	160	165
Thr Lys Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu		
170	175	180
Ile Val Phe Arg Tyr Tyr His Lys Leu Arg Met Ser Val Glu Tyr		
185	190	195
Ser Gln Ser Trp Gly His Phe Gln Asn Arg Val Asn Leu Val Gly		
200	205	210
Asp Ile Phe Arg Asn Asp Gly Ser Ile Met Leu Gln Gly Val Arg		
215	220	225
Glu Ser Asp Gly Gly Asn Tyr Thr Cys Ser Ile His Leu Gly Asn		
230	235	240
Leu Val Phe Lys Lys Thr Ile Val Leu His Val Ser Pro Glu Glu		
245	250	255
Pro Arg Thr Leu Val Thr Pro Ala Ala Leu Arg Pro Leu Val Leu		
260	265	270
Gly Gly Asn Gln Leu Val Ile Ile Val Gly Ile Val Cys Ala Thr		
275	280	285
Ile Leu Leu Leu Pro Val Leu Ile Leu Ile Val Lys Lys Thr Cys		
290	295	300
Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu Val Lys Asn Thr		
305	310	315
Lys Lys Thr Asn Pro Glu Ile Lys Glu Lys Pro Cys His Phe Glu		
320	325	330
Arg Cys Glu Gly Glu Lys His Ile Tyr Ser Pro Ile Ile Val Arg		
335	340	345
Glu Val Ile Glu Glu Glu Glu Pro Ser Glu Lys Ser Glu Ala Thr		
350	355	360
Tyr Met Thr Met His Pro Val Trp Pro Ser Leu Arg Ser Asp Arg		
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Asn Asn Ser Leu Glu Lys Lys Ser Gly Gly Met Pro Lys Thr		
380	385	390
Gln Gln Ala Phe		

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ctctgagctc agttgcagta ctcggaaagc catgcaggat gaagatggat 200

acatcacacctt aaatattaaa actcgaaac cagctctcgt ctccggtggc 250
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 tgcgtgggg atgggtgtcg ggctgggtgc tctggggatt tggctgtca 350
 tgcagcgcaa ttacctacaat gatgagaatg aaaatcgac aggaactctg 400
 caacaattag caaaggcctt ctgtcaatat gtggtaaaac aatcagaact 450
 aaaggcact ttcaaaaggcataaaatgcg cccctgtgac acaaactgga 500
 gatattatgg agatagtcg tatgggttct tcaggcacaa cttAACATGG 550
 gaagagagta a cactgacatc aatgtactc tccctgaatgat 600
 tgacaaccgg aacattgtgg agtacatcaa agccaggact catttaattc 650
 gtgggtcg attatctcg cagaagtgcg atgaggctcg gaagtggag 700
 gatggctcg ttatctcaga aaatatgttt gagttttgg aagatggaaa 750
 agggaaatatg aatttgtgott atttcataa tggggaaatg caccctacct 800
 tctgtgagaa caaacattat ttaatgtgtc agaggaaggc tggcatgacc 850
 aagggtggacc aactaccta atgcaaaagag gtggacagga taacacagat 900
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 aaaaaaaaaaaa aaa 963

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<212> PRT

<213> Homo sapiens

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Lys	Pro	Ala	Leu	Val	Ser	Val	Gly	Pro	Ala	Ser	Ser	Ser	Trp	Trp
				20					25					30

Arg	Val	Met	Ala	Leu	Ile	Leu	Ile	Leu	Cys	Val	Gly	Met	Val
				35				40				45	

Val	Gly	Leu	Val	Ala	Leu	Gly	Ile	Trp	Ser	Val	Met	Gln	Arg	Asn
				50					55			60		

Tyr	Leu	Gln	Asp	Glu	Asn	Glu	Asn	Arg	Thr	Gly	Thr	Leu	Gln	Gln
				65				70				75		

Leu	Ala	Lys	Arg	Phe	Cys	Gln	Tyr	Val	Val	Lys	Gln	Ser	Glu	Leu
				80					85				90	

Lys	Gly	Thr	Phe	Lys	Gly	His	Lys	Cys	Ser	Pro	Cys	Asp	Thr	Asn
				95				100				105		

Trp	Arg	Tyr	Tyr	Gly	Asp	Ser	Cys	Tyr	Gly	Phe	Phe	Arg	His	Asn
				110				115				120		

Leu	Thr	Trp	Glu	Glu	Ser	Lys	Gln	Tyr	Cys	Thr	Asp	Met	Asn	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

125 130 135
Thr Leu Leu Lys Ile Asp Asn Arg Asn Ile Val Glu Tyr Ile Lys
140 145 150
Ala Arg Thr His Leu Ile Arg Trp Val Gly Leu Ser Arg Gln Lys
155 160 165
Ser Asn Glu Val Trp Lys Trp Glu Asp Gly Ser Val Ile Ser Glu
170 175 180
Asn Met Phe Glu Phe Leu Glu Asp Gly Lys Gly Asn Met Asn Cys
185 190 195
Ala Tyr Phe His Asn Gly Lys Met His Pro Thr Phe Cys Glu Asn
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<210> 427

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cagttagcac agcaagtgtc ct 22

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ggcagaaaaatgggaggcaga 19

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<210> 455
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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tgtcagaatg caacctggct t 21

<210> 456
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tgcacctaga tgtccccagc accc 24

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<400> 462
caaattaaag tacccatcg gagagaa 27

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TOP SECRET

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<223> Synthetic oligonucleotide probe

<400> 463
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<210> 464
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<220>
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gggtggaggc tcactgagta ga 22

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<400> 474
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<210> 475
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<210> 482
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<400> 486
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<210> 488
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<210> 493
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gtgggcacgc tcttgtc 17

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cagccgcgc gggagccgga ccgcgcgcgg aggagctcg acggcatgt 150
gagccccctc ctttgctgaa gccccgtgc ggagaagccc gggcaaacgc 200
aggctaagga gaccaaagcg gccaagtcgc gagacagcgg acaagcagcg 250
gaggagaagg aggaggaggc gaacccagag agggcgcga aaagaagcgg 300
tgggtgtggg cgtcgtggc atggcgccg ctatcgccag ctcgctcata 350
cgtcagaaga ggcaagcccc cgagcgcgag aaatccaacg cctgcaagt 400
tgtcagcagc cccagcaaa gcaagaccag ctgcgcacaa aacaagtta 450
atgtctttc cccggcataa ctcttcggc ccaagaagag gcgcagaaga 500
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aggctaccac ttgcagctgc aggccgatgg aaccattgt ggcaccaaaag 600
atgaggacag cacttacact ctgtttaacc tcataccctgt gggtctgcga 650
gtgggtggcta tccaaaggagt tccaaaccaag ctgtacttgg caatgaacag 700
tgagggatac ttgtacacct cggaaactttt cacaccttag tgcaattca 750
aagaatcaat gtttggaaat tattatgtga catattcatc aatgatatac 800
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 gatctcacgg agttctcccg atctggaagc gggaccccaa ccaagagcag 1000
 aagtgtctct ggcgtgctga acggaggcaa atccatgagc cacaatgaat 1050
 caaacgtagcc agtgaggcga aaagaaggcgc tctgtAACAG aacttacct 1100
 ccaggtgctg ttgaattctt cttagcgtcc ttcacccaa agttcaaatt 1150
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 <210> 495
 <211> 245
 <212> PRT
 <213> Homo Sapien

 <400> 495
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 Ala Arg Glu Arg Glu Lys Ser Asn Ala Cys Lys Cys Val Ser Ser
 20 25 30
 Pro Ser Lys Gly Lys Thr Ser Cys Asp Lys Asn Lys Leu Asn Val
 35 40 45
 Phe Ser Arg Val Lys Leu Phe Gly Ser Lys Lys Arg Arg Arg Arg
 50 55 60
 Arg Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu Tyr Ser
 65 70 75
 Arg Gln Gly Tyr His Leu Gln Leu Gln Ala Asp Gly Thr Ile Asp
 80 85 90
 Gly Thr Lys Asp Glu Asp Ser Thr Tyr Thr Leu Phe Asn Leu Ile
 95 100 105
 Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Gln Thr Lys
 110 115 120
 Leu Tyr Leu Ala Met Asn Ser Glu Gly Tyr Leu Tyr Thr Ser Glu
 125 130 135
 Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe Glu Asn
 140 145 150
 Tyr Tyr Val Thr Tyr Ser Ser Met Ile Tyr Arg Gln Gln Gln Ser
 155 160 165
 Gly Arg Gly Trp Tyr Leu Gly Leu Asn Lys Glu Gly Glu Ile Met
 170 175 180
 Lys Gly Asn His Val Lys Lys Asn Lys Pro Ala Ala His Phe Leu
 185 190 195
 Pro Lys Pro Leu Lys Val Ala Met Tyr Lys Glu Pro Ser Leu His
 200 205 210
 Asp Leu Thr Glu Phe Ser Arg Ser Gly Ser Gly Thr Pro Thr Lys

215

220

225

Ser Arg Ser Val Ser Gly Val Leu Asn Gly Gly Lys Ser Met Ser
 230 235 240

His Asn Glu Ser Thr
 245

<210> 496
 <211> 1471
 <212> DNA
 <213> Homo Sapien

<400> 496
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 tgggggatt tcagtaaaa aagtggggta tcccctccat ttagagtcta 200
 gcaaggaaa aaacaccaag gttgggttcc ttccctgacat tggcagtgcc 250
 ccagtagggg tggatgagc gaatattccc aaagctaaag tcccacaccc 300
 tgttagattac aagagtggat ttggcaggag tgcgtccccaa aatacagtgg 350
 aaaggtgcct gaagatattt aaaccacgtc ttggaaattt agtgggttctt 400
 ggctttggaa taggtgaagt gaggacagac actggagagg agggaaagg 450
 gacgttttca ataggaggca aaactcgagg gtgggatcca ctgaggagta 500
 cataggctgc tggatctgtt ggagccagca ctggggccac gggtgtaac 550
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gcctggacaa ggagggccag gtcatgaagg gaaaccgagt taagaagacc 1300
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ccagccacca ccacaacctg t 1471

<210> 497
<211> 225
<212> PRT
<213> Homo Sapien

<400> 497
Met Ala Ala Leu Ala Ser Ser Leu Ile Arg Gln Lys Arg Glu Val
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Arg Glu Pro Gly Gly Ser Arg Pro Val Ser Ala Gln Arg Arg Val
20 25 30
Cys Pro Arg Gly Thr Lys Ser Leu Cys Gln Lys Gln Leu Leu Ile
35 40 45
Leu Leu Ser Lys Val Arg Leu Cys Gly Gly Arg Pro Ala Arg Pro
50 55 60
Asp Arg Gly Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu
65 70 75
Phe Cys Arg Gln Gly Phe Tyr Leu Gln Ala Asn Pro Asp Gly Ser
80 85 90
Ile Gln Gly Thr Pro Glu Asp Thr Ser Ser Phe Thr His Phe Asn
95 100 105
Leu Ile Pro Val Gly Leu Arg Val Val Thr Ile Gln Ser Ala Lys
110 115 120
Leu Gly His Tyr Met Ala Met Asn Ala Glu Gly Leu Leu Tyr Ser
125 130 135
Ser Pro His Phe Thr Ala Glu Cys Arg Phe Lys Glu Cys Val Phe
140 145 150
Glu Asn Tyr Tyr Val Leu Tyr Ala Ser Ala Leu Tyr Arg Gln Arg
155 160 165
Arg Ser Gly Arg Ala Trp Tyr Leu Gly Leu Asp Lys Glu Gly Gln
170 175 180
Val Met Lys Gly Asn Arg Val Lys Thr Lys Ala Ala Ala His
185 190 195
Phe Leu Pro Lys Leu Leu Glu Val Ala Met Tyr Gln Glu Pro Ser
200 205 210
Leu His Ser Val Pro Glu Ala Ser Pro Ser Ser Pro Pro Ala Pro
215 220 225
<210> 498
<211> 744

D991384

<212> DNA
<213> Homo Sapien

<400> 498
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gtgcgcatct tcggcctcaa gaagcgcagg ttgcggcgcc aagatcccc 200
gctcaagggt atatgttacca ggttatattt caggcaaggc tactacttgc 250
aaatgcaccc cgatggagct ctcgatggaa ccaaggatga cagcaactat 300
tctactacttc tcaacactcat accagtggga ctacgtttt ttgcctatcca 350
gggagtggaa acagggttgt atatagccat gaatggagaa ggtaacctt 400
acccatcaga acttttacc cctgaatgc agtttaaaga atctgttttt 450
gaaaattatt atgtaatcta ctcatccatg ttgtacagac aacaggaatc 500
ttgttagagcc ttgtttttgg gattaataaa ggaaggcggaa gctatgaaag 550
ggAACAGAGT aaagaaaacc aaaccagcag ctcattttct acccaagcca 600
ttggaaatgg ccattgttcc agaaccatct ttgcattgtt ttggggaaac 650
ggtcccgaag cctggggtaa cgccaaatggt aagcacaatggt gctgtcgaa 700
taatgttacca aggcaaaacca gtcaacaaga gtaagacaac atag 744

<210> 499
<211> 247
<212> PRT
<213> Homo Sapien

<400> 499
Met Ala Ala Ala Ile Ala Ser Gly Leu Ile Arg Gln Lys Arg Gln
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20 25 30
Ser Ser Pro Ser Lys Asn Arg Gly Leu Cys Asn Gly Asn Leu Val
35 40 45
Asp Ile Phe Ser Lys Val Arg Ile Phe Gly Leu Lys Lys Arg Arg
50 55 60
Leu Arg Arg Gln Asp Pro Gln Leu Lys Gly Ile Val Thr Arg Leu
65 70 75
Tyr Cys Arg Gln Gly Tyr Tyr Leu Gln Met His Pro Asp Gly Ala
80 85 90
Leu Asp Gly Thr Lys Asp Asp Ser Thr Asn Ser Thr Leu Phe Asn
95 100 105
Leu Ile Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Lys
110 115 120

DRAFT

Thr Gly Leu Tyr Ile Ala Met Asn Gly Glu Gly Tyr Leu Tyr Pro
125 130
Ser Glu Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe
140 145 150
Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Met Leu Tyr Arg Gln Gln
155 160 165
Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn Lys Glu Gly Gln
170 175 180
Ala Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro Ala Ala His
185 190 195
Phe Leu Pro Lys Pro Leu Glu Val Ala Met Tyr Arg Glu Pro Ser
200 205 210
Leu His Asp Val Gly Glu Thr Val Pro Lys Pro Gly Val Thr Pro
215 220 225
Ser Lys Ser Thr Ser Ala Ser Ala Ile Met Asn Gly Gly Lys Pro
230 235 240
Val Asn Lys Ser Lys Thr Thr
245
<210> 500
<211> 2906
<212> DNA
<213> Homo Sapien
<400> 500
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gaagctttttt ctgttgagcc ctggatctta acacaatgt gtatatgtgc 200
acacaggagg catccaagaa tgaataaac cagagttaga cccgcgggg 250
ttggtgtgtt ctgcataaaa taaaataatct taagcagct gttccctcc 300
ccacccccc aaaaaaggat gattggaaat gaagaaccga ggattcacaa 350
agaaaaaaagt atgttcattt ttctctataa aggagaaaagt gagccaagga 400
gatattttt gaatgaaaat tttggggctt ttttagtaaa gtaaagaact 450
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aattaataat acatctgcaa agaaattca gagaagaaaa gttgaccgcg 550
gcagatttag gcattgattt ggggagagaa accagcagag cacagtgg 600
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ttcatcaacc tcctttttt taaaattttt ttccctttttt tatcaagatc 700
atgcgttttc tttttttttt aaccacactgg atttccatctt ggttgtgt 750

gtgatcagtc tgaaatacaa ctgttgaat tccagaagga ccaacaccag 800
ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850
ataggctcta ggttaacag ggccttattt gacccctgc ttgtggtgc 900
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gccctctgt gtgcctcgc agcaaccagt tcagcaaggat gatttgtt 1000
cgaaaaacc tgcgtgaggat tccggatggc atctccacca acacacggct 1050
gctgaacctc catgagaacc aaatccagat catcaaagt aacagttca 1100
agcactttag gcaacttggaa atccatcagt tgagtaggaa ccatacaga 1150
accattgaaa ttggggctt caatggctc gcgaacctca acactctgg 1200
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ccaactttag gtatttgaac ctggccatgt gcaacccctcg ggaaatccct 1450
aacctcacac cgctcataaa actagatgag ctggatctt ctggaaatca 1500
tttatctgcc atcaggcctg gctcttcca gggtttgatg cacctcaaa 1550
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cctgacatct gtatcttggta ttactccaa tggacagtc atgacacatg 2000
ggcgatcaca aatgtcggtt gctgtgtca gtatgttgc tttaatttc 2050
acaatgttaa ctgtgcaga tacaggcatg tacacatgtt tggtgatgtt 2100
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agtggtcac tgggagacca ccaatgtgac cacctctc acaccacaga 2300
gcacaaggatc gacagagaaa accttcacca tcccagtgtac tggatataaac 2350

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 catggaaagg cacctgcca tgcctgttat cgagcatgag cacctaaatc 2600
 actataact atacaaaatct cccttcaacc acacaacaac agttaacaca 2650
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 caaaaa 2906

 <210> 501
 <211> 640
 <212> PRT
 <213> Homo Sapien

 <400> 501

Met	Leu	Asn	Lys	Met	Thr	Leu	His	Pro	Gln	Gln	Ile	Met	Ile	Gly
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Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
		20							25					30

Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
			35					40						45

Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
				50				55						60

Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
				65				70						75

Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	Glu	Asn	Gln	Ile	Gln	Ile	
				80				85						90

Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Ile	Arg	His	Leu	Glu	Ile	Leu
				95				100						105

Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
				110				115						120

Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
				125				130						135

Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
				140				145						150

Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser
				155				160						165

Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly
 170 175 180
 Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly
 185 190 195
 Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg
 200 205 210
 Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp
 215 220 225
 Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln
 230 235 240
 Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile
 245 250 255
 Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val
 260 265 270
 Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp
 275 280 285
 Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His
 290 295 300
 Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp
 305 310 315
 Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys
 320 325 330
 Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp
 335 340 345
 Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro
 350 355 360
 Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys
 365 370 375
 Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn
 380 385 390
 Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val
 395 400 405
 Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp
 410 415 420
 Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
 425 430 435
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro
 440 445 450
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
 455 460 465
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
 470 475 480

Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
485 490 495

Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
500 505 510

Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
515 520 525

Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
530 535 540

Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
545 550 555

Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
560 565 570

Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
575 580 585

Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
590 595 600

Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn
605 610 615

Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn
620 625 630

Ser Lys Asp Asn Val Gln Glu Thr Gln Ile
635 640

<210> 502
<211> 2458
<212> DNA
<213> Homo Sapien

<400> 502
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ccagactcgcc cgagggtccgt cggaggcgcc cggccgcggcc ggagccaagc 150
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caactggggc ttccagaaaa agacactctg gatattgaat ggctgtcac 350
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gagtttggaaag gagagactgac agaaggaagt gacctgactt tgcagtgtga 650
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cctcaaatca gatgcctctaa aggactttcc tgcttagatat ttctggaaagg 2150
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<210> 503
 <211> 373
 <212> PRT
 <213> Homo Sapien

<400>	503													
Met	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Val	Ser	Tyr	Tyr	Val	Gly	
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Thr	Leu	Gly	Thr	His	Thr	Glu	Ile	Lys	Arg	Val	Ala	Glu	Glu	Lys
	20							25					30	
Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp
			35					40					45	
Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln
		50						55					60	
Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu
		65						70					75	
Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu
		80						85					90	
Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp
		95						100					105	
Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val
		110						115					120	
Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro
		125						130					135	
Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr
		140						145					150	
Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr
		155						160					165	
Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro
		170						175					180	
Pro	Lys	Ser	Arg	Ile	Asp	Tyr	Asn	His	Pro	Gly	Arg	Val	Leu	Leu
		185						190					195	
Gln	Asn	Leu	Thr	Met	Ser	Tyr	Ser	Gly	Leu	Tyr	Gln	Cys	Thr	Ala
		200						205					210	
Gly	Asn	Glu	Ala	Gly	Lys	Glu	Ser	Cys	Val	Val	Arg	Val	Thr	Val
		215						220					225	

Gln Tyr Val Gln Ser Ile Gly Met Val Ala Gly Ala Val Thr Gly
 230 235 240
 Ile Val Ala Gly Ala Leu Leu Ile Phe Leu Leu Val Trp Leu Ile
 245 250 255
 Ile Arg Arg Lys Asp Lys Glu Arg Tyr Glu Glu Glu Glu Arg Pro
 260 265 270 270
 Asn Glu Ile Arg Glu Asp Ala Glu Ala Pro Lys Ala Arg Leu Val
 275 280 285
 Lys Pro Ser Ser Ser Ser Gly Ser Arg Ser Ser Arg Ser Gly
 290 295 300
 Ser Ser Ser Thr Arg Ser Thr Ala Asn Ser Ala Ser Arg Ser Gln
 305 310 315
 Arg Thr Leu Ser Thr Asp Ala Ala Pro Gln Pro Gly Leu Ala Thr
 320 325 330
 Gln Ala Tyr Ser Leu Val Gly Pro Glu Val Arg Gly Ser Glu Pro
 335 340 345
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 350 355 360
 Ser Met Ile Pro Ser Gln Ser Arg Ala Phe Gln Thr Val
 365 370

 <210> 504
 <211> 3060
 <212> DNA
 <213> Homo Sapien

 <400> 504
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 ctctctgtcgat gagtagtggaa tttcgccaga agtttgatgtat tcaactactcc 150
 tgaagagatg attaaaaaag ccaaaaggaa aactgcctat ctggccatgc 200
 aatttacgtt tagtccccaa gaccaggaa gctgtggatcatcgatggct 250
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 ttggagacaaa attttatgtatg actactatcc agatctgaaatggccgatgtac 350
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 aatttacaac tggcagatat tggccatcatat cagtgcaaaatggcc 450
 tcctgggtttt gcaaataaga agattcatct ggttttttctt gttaaggctt 500
 caggtgcgatgtt atgttacgtt gatggatctg aagaaattgg aagtgtactt 550
 aagataaaaatgttacccaa agaagggttca cttccattac agttagatgt 600
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<210> 505
<211> 352
<212> PRT
<213> Homo Sapien

<400> 505
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Lys Ala Lys Gly Glu Thr Ala Tyr Leu Pro Cys Lys Phe Thr Leu
35 40 45
Ser Pro Glu Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Ile Ser
50 55 60
Pro Ala Asp Asn Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser
65 70 75
Gly Asp Lys Ile Tyr Asp Asp Tyr Tyr Pro Asp Leu Lys Gly Arg
80 85 90
Val His Phe Thr Ser Asn Asp Leu Lys Ser Gly Asp Ala Ser Ile
95 100 105
Asn Val Thr Asn Leu Gln Leu Ser Asp Ile Gly Thr Tyr Gln Cys
110 115 120
Lys Val Lys Lys Ala Pro Gly Val Ala Asn Lys Lys Ile His Leu

	125		130		135
Val Val Leu Val Lys Pro Ser Gly Ala Arg Cys Tyr Val Asp Gly					
140			145		150
Ser Glu Glu Ile Gly Ser Asp Phe Lys Ile Lys Cys Glu Pro Lys					
155			160		165
Glu Gly Ser Leu Pro Leu Gln Tyr Glu Trp Gln Lys Leu Ser Asp					
170			175		180
Ser Gln Lys Met Pro Thr Ser Trp Leu Ala Glu Met Thr Ser Ser					
185			190		195
Val Ile Ser Val Lys Asn Ala Ser Ser Glu Tyr Ser Gly Thr Tyr					
200			205		210
Ser Cys Thr Val Arg Asn Arg Val Gly Ser Asp Gln Cys Leu Leu					
215			220		225
Arg Leu Asn Val Val Pro Pro Ser Asn Lys Ala Gly Leu Ile Ala					
230			235		240
Gly Ala Ile Ile Gly Thr Leu Leu Ala Leu Ala Leu Ile Gly Leu					
245			250		255
Ile Ile Phe Cys Cys Arg Lys Lys Arg Arg Glu Glu Lys Tyr Glu					
260			265		270
Lys Glu Val His His Asp Ile Arg Glu Asp Val Pro Pro Pro Lys					
275			280		285
Ser Arg Thr Ser Thr Ala Arg Ser Tyr Ile Gly Ser Asn His Ser					
290			295		300
Ser Leu Gly Ser Met Ser Pro Ser Asn Met Glu Gly Tyr Ser Lys					
305			310		315
Thr Gln Tyr Asn Gln Val Pro Ser Glu Asp Phe Glu Arg Thr Pro					
320			325		330
Gln Ser Pro Thr Leu Pro Pro Ala Lys Phe Lys Tyr Pro Tyr Lys					
335			340		345
Thr Asp Gly Ile Thr Val Val					
350					

<210> 506
<211> 1705
<212> DNA
<213> Homo Sapien

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ccagctgcct ccaggcagcc agccctcaag catcaattac aggaccagag 150
ggacaagaca tgactgttat gagggagctgc tttcgccaat ttaacccaaa 200
qaagaatttaa ggctgttgg gaggaaaggcc aggaggaaca cgagacttag 250
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ttctgcctc ctttgctgc gacagccctt caaatgcaga tggtgtgtct 350
cccttgcctg ggttttaccc tgcttctctg gagccaggtt tcagggggcc 400
agggccaaga attccacttt gggccctgcg aagtgaaggg ggttgttccc 450
cagaaaactgt gggaaaggctt ctgggctgtg aaagacacta tgcaagctca 500
ggataaacatc acgagtgccc ggctgctgcg gcaggagggtt ctgcagaacg 550
tctcgatgc tgagagctgt taccttgtcc acaccctgtt ggagttctac 600
ttgaaaactg ttttcaaaaa ccaccacaaat agaacagttt aagtcaaggac 650
tctgaagtca ttctctactc tggccaaacaa ctttgttctc atcgtgtcac 700
aactgcaacc cagtcaagaa aatgagatgt tttccatcg agacagtgc 750
cacaggcggtt ttctgctatt ccggagagca ttcaaacagt tggacgtaga 800
agcagctctg accaaagccc ttgggaaagt ggacattttt ctgacactgga 850
tgcaaaaaattt ctacaagctc tgaatgtcta gaccaggacc tccctcccc 900
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cttcttacc cctcacaatc cttgccacag tggggccag tggatgggtg 1250
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ccctgctaat aaaagacaac ataactccaa aaaaaaaaaa aaaaaaaaaa 1700
aaaaaa 1705

<210> 507
<211> 206
<212> PRT

<213> Homo Sapien

<400> 507

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Pro	Phe	Cys	Pro	Pro	Leu	Leu	Ala	Thr	Ala	Ser	Gln	Met		
				20				25						30
Val	Val	Leu	Pro	Cys	Leu	Gly	Phe	Thr	Leu	Leu	Leu	Trp	Ser	Gln
				35				40						45
Val	Ser	Gly	Ala	Gln	Gly	Gln	Glu	Phe	His	Phe	Gly	Pro	Cys	Gln
				50				55						60
Val	Lys	Gly	Val	Val	Pro	Gln	Lys	Leu	Trp	Glu	Ala	Phe	Trp	Ala
				65				70						75
Val	Lys	Asp	Thr	Met	Gln	Ala	Gln	Asp	Asn	Ile	Thr	Ser	Ala	Arg
				80				85						90
Leu	Leu	Gln	Gln	Glu	Val	Leu	Gln	Asn	Val	Ser	Asp	Ala	Glu	Ser
				95				100						105
Cys	Tyr	Leu	Val	His	Thr	Leu	Leu	Glu	Phe	Tyr	Leu	Lys	Thr	Val
				110				115						120
Phe	Lys	Asn	His	His	Asn	Arg	Thr	Val	Glu	Val	Arg	Thr	Leu	Lys
				125				130						135
Ser	Phe	Ser	Thr	Leu	Ala	Asn	Asn	Phe	Val	Leu	Ile	Val	Ser	Gln
				140				145						150
Leu	Gln	Pro	Ser	Gln	Glu	Asn	Glu	Met	Phe	Ser	Ile	Arg	Asp	Ser
				155				160						165
Ala	His	Arg	Arg	Phe	Leu	Leu	Phe	Arg	Arg	Ala	Phe	Lys	Gln	Leu
				170				175						180
Asp	Val	Glu	Ala	Ala	Leu	Thr	Lys	Ala	Leu	Gly	Glu	Val	Asp	Ile
				185				190						195
Leu	Leu	Thr	Trp	Met	Gln	Lys	Phe	Tyr	Lys	Leu				
				200				205						

<210> 508

<211> 924

<212> DNA

<213> Homo Sapien

<400> 508

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cggtctcagg	agatgtctga	tttccacaga	catgcacca	atagaagaga	150
gtttccaaga	aatcaaaga	gccatccaa	ctaaggacac	cttcccaaat	200
gtcactatcc	tgtccacatt	ggagactctg	cagatcatta	agccccttaga	250
tgtgtgtcgc	gtgaccaaga	acctctggc	gttctacgtg	gacagggtgt	300

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 aatgttctca gcttgatgac aaggaacctg tatagtgatc cagggatgaa 600
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 taaactctat ctgctgaaag ggcctgcagg ccacccctggg agtaaaggc 800
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<210> 509

<211> 177

<212> PRT

<213> Homo Sapien

<400> 509
 Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu
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 Ile Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile
 20 25 30
 Ser Thr Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys
 35 40 45
 Arg Ala Ile Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu
 50 55 60
 Ser Thr Leu Glu Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys
 65 70 75
 Cys Val Thr Lys Asn Leu Leu Ala Phe Tyr Val Asp Arg Val Phe
 80 85 90
 Lys Asp His Gln Glu Pro Asn Pro Lys Ile Leu Arg Lys Ile Ser
 95 100 105
 Ser Ile Ala Asn Ser Phe Leu Tyr Met Gln Lys Thr Leu Arg Gln
 110 115 120
 Cys Gln Glu Gln Arg Gln Cys His Cys Arg Gln Glu Ala Thr Asn
 125 130 135
 Ala Thr Arg Val Ile His Asp Asn Tyr Asp Gln Leu Glu Val His
 140 145 150
 Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu Asp Val Phe Leu Ala

155

160

165

Trp Ile Asn Lys Asn His Glu Val Met Phe Ser Ala
 170 175

<210> 510
 <211> 996
 <212> DNA
 <213> Homo Sapien

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 tccacagggt tccactccca ggtccaaactg cacctcggtt ctatcgataa 200
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<210> 511
 <211> 251
 <212> PRT
 <213> Homo Sapien

<400> 511
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 Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
 20 25 30

Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala
35 40 45
Thr Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His
50 55 60
Val Asp Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile
65 70 75
Arg Ser Glu Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser
80 85 90
Arg Arg Tyr Leu Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser
95 100 105
His Tyr Phe Asp Pro Glu Asn Cys Arg Phe Gln His Gln Thr Leu
110 115 120
Glu Asn Gly Tyr Asp Val Tyr His Ser Pro Gln Tyr His Phe Leu
125 130 135
Val Ser Leu Gly Arg Ala Lys Arg Ala Phe Leu Pro Gly Met Asn
140 145 150
Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg Arg Asn Glu Ile Pro
155 160 165
Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg His Thr Arg Ser
170 175 180
Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val Leu Lys Pro
185 190 195
Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln Glu Leu
200 205 210
Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu Gly
215 220 225
Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
230 235 240
Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
245 250

<210> 512
<211> 2015
<212> DNA
<213> Homo Sapien

<400> 512
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ctgctggag gttgggggtct ctgggagctc tgccaggcccc agcacccgca 150
gagcagacac tgcgatgaca acggacgaca cagaagtgcc cgctatgact 200
ctagcacccgg gccacgccc tctggaaact caaacgtga gcgctgagac 250
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acatctccca acttcatggt gctgatcgcc acctccgtgg agacatcgc 400
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cagccgcctc tccgacggc cccatccagt catcaccccg tcatggtccc 750
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catccctggg gcctcagaca tagatctcat ccccacggaa ggggtgaagg 900
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ggtgtccttg gactcacctt ggcacatgtt ctgtgtttca gtaaagagag 1950
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<210> 513
<211> 482
<212> PRT
<213> Homo Sapien

<400> 513

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20 25 30

Arg Ala Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala
35 40 45

Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu
50 55 60

Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Ile
65 70 75

Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg
80 85 90

Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val Leu
95 100 105

Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu
110 115 120

Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro
125 130 135

Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu
140 145 150

Glu Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr
155 160 165

Ser Thr Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser
170 175 180

Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser
185 190 195

Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg
200 205 210

Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile
215 220 225

Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu Ala Glu
230 235 240

Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser Ile
245 250 255

Thr Glu Ile Glu Thr Thr Ser Ser Ile Pro Gly Ala Ser Asp
 260 265 270
 Ile Asp Leu Ile Pro Thr Glu Gly Val Lys Ala Ser Ser Thr Ser
 275 280 285
 Asp Pro Pro Ala Leu Pro Asp Ser Thr Glu Ala Lys Pro His Ile
 290 295 300
 Thr Glu Val Thr Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly Thr
 305 310 315
 Thr Glu Ser Ala Ala Pro His Ala Thr Val Gly Thr Pro Leu Pro
 320 325 330
 Thr Asn Ser Ala Thr Glu Arg Glu Val Thr Ala Pro Gly Ala Thr
 335 340 345
 Thr Leu Ser Gly Ala Leu Val Thr Val Ser Arg Asn Pro Leu Glu
 350 355 360
 Glu Thr Ser Ala Leu Ser Val Glu Thr Pro Ser Tyr Val Lys Val
 365 370 375
 Ser Gly Ala Ala Pro Val Ser Ile Glu Ala Gly Ser Ala Val Gly
 380 385 390
 Lys Thr Thr Ser Phe Ala Gly Ser Ser Ala Ser Ser Tyr Ser Pro
 395 400 405
 Ser Glu Ala Ala Leu Lys Asn Phe Thr Pro Ser Glu Thr Pro Thr
 410 415 420
 Met Asp Ile Ala Thr Lys Gly Pro Phe Pro Thr Ser Arg Asp Pro
 425 430 435
 Leu Pro Ser Val Pro Pro Thr Thr Asn Ser Ser Arg Gly Thr
 440 445 450
 Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys Thr Thr Met
 455 460 465
 Lys Pro Gln Gln Pro Arg Pro Arg Leu Pro Gly Arg Gly Arg Pro
 470 475 480

Gln Thr

<210> 514
 <211> 2284
 <212> DNA
 <213> Homo Sapien

<400> 514
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 ggcgcggggg tcctctcgac gccagagaga aatctcatca tctgtgcgc 150
 cttcttaaag caaactaaga ccagaggagg gattatcctt gacctttgaa 200
 gaccaaaaact aaactgaaat taaaatgtt ctgcggggaa gaaggggagct 250

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acccaactgc tacctatccc tctgtccca cgagggagcc tgtccattga 550
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<210> 515

<211> 431

<212> PRM

<213> Homo Sapien

<400> 515
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35 40 45
Ser Lys Gly Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln
50 55 60
Glu Asp Cys Ile Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly
65 70 75
Asp Lys Ala Cys Asn Leu Met Ile Phe Asp Thr Arg Lys Thr Ala
80 85 90
Arg Gln Pro Asn Cys Tyr Leu Phe Cys Pro Asn Glu Ala
95 100 105
Cys Pro Leu Lys Pro Ala Lys Gly Leu Met Ser Tyr Arg Ile Ile
110 115 120
Thr Asp Phe Pro Ser Leu Thr Arg Asn Leu Pro Ser Gln Glu Leu
125 130 135
Pro Gln Glu Asp Ser Leu Leu His Gly Gln Phe Ser Gln Ala Val
140 145 150
Thr Pro Leu Ala His His His Thr Asp Tyr Ser Lys Pro Thr Asp
155 160 165
Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly Ser Ser Asp
170 175 180
His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala Gln Leu
185 190 195

Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe Ser
200 205 210
Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala
215 220 225
Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala
230 235 240
Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr
245 250 255
Pro Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro
260 265 270
Val Thr Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr
275 280 285
Val Phe Thr Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr
290 295 300
Ala Val Leu Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly
305 310 315
Ser Leu Glu Thr Ile Pro Phe Thr Glu Ile Ser Asn Leu Thr Leu
320 325 330
Asn Thr Gly Asn Val Tyr Asn Pro Thr Ala Leu Ser Met Ser Asn
335 340 345
Val Glu Ser Ser Thr Met Asn Lys Thr Ala Ser Trp Glu Gly Arg
350 355 360
Glu Ala Ser Pro Gly Ser Ser Ser Gln Gly Ser Val Pro Glu Asn
365 370 375
Gln Tyr Gly Leu Pro Phe Glu Lys Trp Leu Leu Ile Gly Ser Leu
380 385 390
Leu Phe Gly Val Leu Phe Leu Val Ile Gly Leu Val Leu Leu Gly
395 400 405
Arg Ile Leu Ser Glu Ser Leu Arg Arg Lys Arg Tyr Ser Arg Leu
410 415 420
Asp Tyr Leu Ile Asn Gly Ile Tyr Val Asp Ile
425 430

<210> 516
<211> 2749
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 1869, 1887
<223> unknown base

<400> 516
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0
5
8
7
6
5
4
3
2
1
0

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gacctttta taaataaaaat gttcatcagc tgcataaaaaa aaaaaaaaaa 2749

<210> 517
<211> 332
<212> PRT
<213> Homo Sapien

<400> 517
Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly
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Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly
20 25 30
Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp
35 40 45
His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg
50 55 60
Cys Ser Gly Thr Ile Tyr Ala Glu Glu Gly Gln Glu Thr Met
65 70 75

Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu
 80 85 90
 Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr
 95 100 105
 Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile
 110 115 120
 Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser
 125 130 135
 Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala
 140 145 150
 Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu
 155 160 165
 Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu
 170 175 180
 Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr
 185 190 195
 Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro
 200 205 210
 Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala
 215 220 225
 Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg
 230 235 240
 Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu
 245 250 255
 Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His
 260 265 270
 Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln
 275 280 285
 Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys
 290 295 300
 Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro
 305 310 315
 Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val
 320 325 330
 Ser Ala

<210> 518
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 518

ccctgcagt cacctacagg gaag 24
<210> 519
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 519
ctgtcttccc ctgcttgct gtgg 24

<210> 520
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 520
ggtcaggaa gggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 521
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 521
ccagtgcaca gcaggcaacg aagc 24

<210> 522
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 522
actaggctgt atgcctgggt gggc 24

<210> 523
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 523
gtatgtacaa agcatcgcca tggttgcagg agcagtgaca ggc 43

<210> 524
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 524
aatctcagca ccagccactc agagca 26

<210> 525

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 525
gttaaaggagg gtgccttcc agcga 25

<210> 526

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 526
tatcccaatg cttccccact gctc 24

<210> 527

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 527
gatgaacctg gcgaaggggc ggca 24

<210> 528

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 528
aggaggatt atcccttgacc tttgaagacc 30

<210> 529

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 529

gaagcaagtg cccagtc 18

<210> 530

<211> 18

<212> DNA

<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe
<400> 530
cgggtccctg ctctttgg 18
<210> 531
<211> 24
<212> DNA
<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe
<400> 531
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<210> 532
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 532
agtgttaagtc aagctccc 18